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GenCore version 5.1.6
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April 29, 2004, 08:37:12 ; Search time 50.5 Seconds (without alignments) 615.450 Million cell updates/sec protein search, using sw model • OM protein Run on:

US-09-674-857-12 583 Title: Perfect score:

1 APPVAGGPSVFLFPPKPKDT......CKVSNKGLPSSIEKTISKAK 110 Sequence:

BLOSUM62

Scoring table:

1586107 seqs, 282547505 residues Gapop 10.0 , Gapext 0.5 Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 29Jan04:*

1: geneseq11980s:*

2: geneseq1990s:*

4: geneseq2000s:*

5: geneseq2001s:*

6: geneseq2003s:*

7: geneseq2003as:*

7: geneseq2003as:*

8: geneseq2003as:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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core Match Length	Leng	the state of	DB	DI	Description
5 97.2 46	4	. 7	2	AAW14933	Aaw14933 2A2 (Chim
97.		N	N	AAW14934	Aaw14934 2A2 (Chim
97.2 46	46	~	۲3	AAW14939	Aaw14939 3F4 (Chim
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97.2 47	47	N	'n	ABP51695	ភ
96.9	110	_		AAR41717	<u></u>
96.9	218			AAB07478	Aab07478 Amino aci
96.9	218			AAB76425	Aab76425 Human 1gG
96.9	218			AAB67205	Human
96.9	218			AAG78436	Aag78436 Native se
96.9	218		9	ABR42442	
96.9	229		۲-	ADD32013	3 Heter
96.9	284		9	AAE30927	~
96.9	327		N	AAW37346	9
96.9	327		Ŋ	AAM47859	Aam47859 Human Ig-
96.9	327		9	AAE32918	Aae32918 Human imm
6.96	327		9	AAE32630	Aae32630 Human imm
36.9	327			AAO30892	
96.9	329			AAW70801	Aaw70801 Amino aci
96.9	329			AAY92190	0
96.9	330			ABR42735	Anti-t
96.9	382			AAR90922	Aar90922 IL4.Y124D
65 96.9 382	ω		N	AAR90921	Aar90921 IL4.Y124D
96.9	σ,		7	AAW10534	Aaw10534 Leptin 1-
96.9 39	38	10	N	AAW10535	Aaw10535 Leptin 1-

Hetero	_		Humari	2 Human 1gG	2 Amino aci	4 Protein s	4	2 Muri	5 2A2	_	8 Murine an	m	7 Anti-huma	7 Human gam	ın	6 Human ga	1 Gamma	3 Gamma 4 h	9 Gamma 4	
0.1	9	Aaw1857	Φ	Aay3167	Abr5534	Adc7323	Abp9629	Aaw1493	Aaw1493	Aaw1494	Aaw1493	Add9378	Aar80617	Aaw1492	Aaw1492	Aaw1492	Ade3159	Ade3159:	Ade3158	
ADD32018	AAY17903	AAW18579	AAW13564	AAY31672	ABR55342	ADC73234	ABP96294	AAW14932	AAW14935	AAW14941	AAW1493B	ADD93783	AAR80617	AAW14927	AAW14925	AAW14926	ADE31591	ADE31593	ADE31589	
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96.9		6.96	96.9	6.96	96.9	6.96		6.96	6.96	96.9	96.9			6.96		6.96		6.96	6.96	
565	565	565	565	565	565	565	565	565	565	565	565	565	565	565	565	565	565	365	565	
26	27	28	29	30	31	32	33	34	35	36	37	38	39	4	41	42	43	44	45	

ALIGNMENTS

RESULT 1

AAW1	
G	AAW14933 standard, protein; 462 AA.
X	
AC	AAW14933;
X	
DT	17-OCT-2003 (revised)
Ţ	16-JUN-1997 (first entry)
X	
DE	2A2 (Chimeric) human G2/G4 chimeric antibody.
×	
KW	Xenotransplantation; graft rejection; cell interaction; pig;
×	vascular cell adhesion molecule; VCAM; monoclonal antibody;
Ž	chimeric antibody; diagnosis.
×	
S	Homo; sapiens.
8	Mus sp.
8	Chimeric
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PN	WO9711971-A1.
X	
ΒD	03-APR-1997.
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ם	27-SEP-1996; 96WO-US015575.
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PR	28-SEP-1995; 95US-0004489P.
PR	26-SEP-1996; 96US-00004489.
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PA	(ALEX-) ALEXION PHARM INC.
×	
ΡΙ	Mueller JP, Evans MJ, Mueller BE, Rollins S, Rother RP, 1
×	
DR	WPI; 1997-212855/19.

WFI; 1997-414655, N-PSDB; AAT62931

Matis LA;

Antibodies binding to porcine but not human cell interaction proteins useful to treat and assay for rejection of xenografted porcine organs, tissues or cells.

Disclosure; Page 42-44; 105pp; English.

A chimeric antibody (AAW14933) comprises the C1 and hinge regions of human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 MAb) and a murine anti-porcine soluble vascular cell adhesion molecule (VCAM) monocolonal antibody (MAb) 2A2 heavy chain variable region sequence (see also AAW14932). The chimeric antibody is specific for porcine VCAM. It is useful for diagnosing human rejection of porcine xenotransplants and for improving xenotransplantation of porcine cells, tissues and organs into

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APPVAGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQBDPEVQFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                           sapiens
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26-SEP-1996;
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16-JUN-1997
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                                                                                                                                        AAW14939;
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                                                                                    1 APPVAGGPSVFLFPPKPKDTLMISRTPEVICVVVDVSQBDPEVQFNWYVDGVEVHNAKIK
                                                                Gaps
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 (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                             PREBOPNSTYRVVSVLTVLHODWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                       306 PREEQFINSTYRVUSVLTVIAQDWINGKEYKCKVSNKGLPSSIEKTISKAK 355
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                                           Length 462;
                                                                                                                                                                                                                                                                                                 Xenotransplantation; graft rejection; cell interaction; pig; vascular cell adhesion molecule; VCAM; monoclonal antibody; chimeric antibody; diagnosis.
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                                                               Indels
                                         97.2%; Score 566.5; DB 2; 99.1%; Pred. No. 1.2e-48; ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                               2A2 (Chimeric) human G2/G4 chimeric antibody.
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                                                                                                                                                                                                      AAW14934 standard, protein; 462
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                                                               Conservative
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                                                    Local Similarity
Les 109, Conser
  human recipients.
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                     Sequence 462 AA;
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16-JUN-1997
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Matches
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97.2%; Score 566.5; DB 2; Length 462; 99.1%; Pred. No. 1.2e-48; ive 0; Mismatches 0; Indels 1.

Best Local Similarity 99.1 Matches 109; Conservative

Query Match

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247 APPVA_GPSVFLFPPPKPXDTLÆISRTPEVTCVV/DVSQEDFEVQENWYVDGVEVHNAKTK 305
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                                                                                 PREEQFINSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                    PREBQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenotransplantation; graft rejection; cell interaction; pig; vascular cell adhesion molecule; VCAM; monoclonal antibody; chimeric antibody; diagnosis.
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llarity 99.1%; Pred. No. 1.2e-48;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                             AAW14939 standard; protein; 463
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N-PSDB; AAT62936.
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A chimeric antibody (AAW14940) comprises the C1 and hinge regions of human 19G2 and the C2 and C3 regions of human 19G4 (G2/G4 MAb) and a murine anti-porcine soluble vascular cell adhesion molecule (VCAM) monoclonal antibody (MAb) 3F4 heavy chain variable region sequence [see also AAW14938). The chimeric antibody is specific for porcine VCAM. It is useful for diagnosing human rejection of porcine exentransplants and for improving xenotransplants and for human recipients. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Evans MJ, Mueller EE, Rollins S, Rother RP, Matis LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibodies binding to porcine but not human ceil interaction proteins useful to treat and assay for rejection of xenografted porcine organs, tissues or cells.
                                                                                                                                                           Xenotransplantation; graft rejection; cell interaction; pig vascular cell adhesion molecule; VCAM; monoclonal antibody; chimeric antibody; diagnosis.
                                                                                                                                3F4 (Chimeric) human G2/G4 chimeric antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 58-61; 105pp; English.
                            AAW14940 standard; protein; 463 AA.
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96US-00004489.
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26-SEP-1996;
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16-JUN-1997
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RESULT 4
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1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                1; Gaps
                                                                                                                         61 PREBOFNSTYRVVSVLTVLHODWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                             97.2%; Score 566.5; DB 2; Length 463; 99.1%; Pred. No. 1.2e-48; ive 0; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                      ABP51695 standard; protein; 472 AA.
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               Best Local Similarity 99.1
Matches 109; Conservative
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RESULT 6

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The present invention describes an immunoglobin molecule or its fragment [1] comprising a region where amino acid residues corresponding to at least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoietin (BPO) or thrombopoietin (TPO) mimetic, that is flanked with proline at its carboxy terminus. (I) has an entianaemic, haemostatic and nephtorropic activities, and can be used as a stimulator of proliferation, differentiation and maturation of haematopoietic cells, and a stimulator of proliferation, differentiation or growth of promegakaryocytes or megakaryocytes, where (I) is contacted with promegakaryocytes or megakaryocytes, where (I) is contacted with promegakaryocytes or megakaryocytes, which results in increasing to production of CDR is replaced with a RPO mimetic, or which has one or a portion of CDR is replaced with an BPO mimetic, or which has one or production of red blood cells, where (I) is contacted with has meet the production of red blood cells, where (I) is contacted with has meet contacted in cell isolation strategies, and for treating patients therefore the appreciation of the suppression of haematopoiesis.

**ABQ71578** to ABQ71578** t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A novel immunogen molecule comprising a region in which amino acid residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoietin or thrombopoetin mimetic.
                                                                        TPO; BPO; thrombopoietin; erythropoietin; antibody; CDR region; complementarity determining region; immunoglobin; antianaemic; haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PREEQFINSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.2%; Score 566.5; DB 5; Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,2e-48;
na 0; Indels
                       5G1.1-TPO heavy chain amino acid sequence SEQ ID NO:67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barbas-Frederickson S, Renshaw M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.1%; Pred. No. 1.26 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Fig 13A; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            05-DEC-2000; 2000US-0251448P.
04-MAY-2001; 2001US-0288889P.
29-MAY-2001; 2001US-0294068P.
                                                                                                                                                                                                                                                                                                                                                                           05-DEC-2001; 2001WO-US047656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ALEX-) ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               al Similarity 99.1
109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-566610/60.
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                                                                                                                                                                                                                                                                  WO200246238-A2.
                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bowdish KS,
                                                                                                                                                                                                                                                                                                                         13-JUN-2002.
                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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8
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AABO7474-78 represent native IgG Fc regions. The proteins are used to produce Fc region-containing polypeptides that have altered effector function as a consequence of one or more amino acid modifications in the Fc region. The variant polypeptides are useful for treating cancer, allergic conditions such as asthma (with an anti-lgE antibody), and LFA-1-mediated disorders. Where the polypeptide binds the HER2 receptor, the disorder preferably is HER2-expressing cancer, e.g. a benign or malignant tumour characterized by overexpressing cancer, small-cell lung cancer, gastrointestinal cancer, pancreatic cancer, ploblastoma, cervical cancer, overian cancer, plander cancer, color cancer, color cancer, colorectal cancer, overian cancer, bladder cancer, nepatoma, carcinoma, kidney cancer, liver cancer, prostate cancer, valval cancer, thyroid cancer, hepatic carcinoma and various types of head and neck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Fc region-containing polypeptides that have altered effector function due to one or more amino acid modifications in the Fc region, useful in the treatment of cancer and allergic conditions such as asthma.
                                                                                                                                                         IgG antibody; light chain; Fc region; effector function; cancer; allergy; asthma; LFA-1-mediated disorder; tumour; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 APPVAGGDSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PREEQENSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.9%; Score 565; DB 3; Length 21 llarity 97.3%; Pred. No. 6.9e-49; Conservative 0; Mismatches 3; Indels
                                                                                                                  Amino acid sequence of native IgG Fc region humIgG4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human IgG4 Fc region amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 22A; 132pp, English
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                                                                                                                                                                                                                                                                                                                                                                                         14-JAN-2000; 2000WO-US000973.
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                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-476035/41.
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les 107; Conserv
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                                                                                                                                                                                                                                                                                           WO200042072-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JAN-1999;
                                                                                                                                                                                                                                            Homo sapiens.
                                                                      20-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Presta LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                    AAB07478;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
슝
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128.1 is an anti-human transferrin receptor antibody which binds to the transferrin receptor on brain capillary endothelial cells. This autibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent or diagnostic agent. The conjugate may be used to treat or prevent conventional disorders eg. brain tumours, AIDS, stroke, epilepsy, parkinsons and Alzaeimers disease. It may also be used for diagnostic methods. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                               chain reaction; primer; PCR; amplify; murine; pAH4625; heavy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 APEFLGGPSVFLFPPKKDTLAISRTPEVTCVVVDVSQEDPEVQFNMYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                    light; chain, variable; constant; region; anti-human; pAH4807; transferrin; receptor; antibody; brain; capillary; pAH4808; gamma-2; endothelial cell; conjugate; neuropharmaceutical; gamma-3; gamma-4; diagnostic; agent; tumour; AIDS; stroke; epilepsy; monoclonal; Parkinsons disease; Alzheimers disease; SP2/0 cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ugates specific for transferrin receptor - used for treatment of cancer, AIDS and neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIBKTISKAK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.9%; Score 565; DB 2; Length 110; 97.3%; Pred. No. 3.1e-49; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                Undefined ORF2 encoded by plasmid pAH4808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 19J; 151pp; English.
                          AAR41717 standard; protein; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92WO-US010206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91US-00800458
                                                                                                                          (revised)
(first entry)
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Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ALKE-) ALKERMES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1993-196742/24.
N-PSDB; AAQ43848.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody conjugates
diagnosis and treatm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9310819-A1
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                                                                                                                       25-MAR-2003
20-0CT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JUN-1993.
                                                                                                                                                                                                                                                 Polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Friden PM;
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Best Local S
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9 61

AA307478 standard; protein; 218 AA

RESULT 7 AAB07478

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Length 218;

02-JUL-1999; 99US-0142088P. 30-JUN-2000; 2000WO-US018185.

Dennis MS, Lazarus RA; (GETH) GENENTECH INC

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This invention relates to non-naturally occurring peptide ligands which bind to the human erbB2 gene product ErbB2 (also known as HER2). Peptides represented in AB47630 - AB476420 and AB476432 - AB476409. Peptides of the ErbB2 binding ligands of the invention. Sequences AB476421 - AB576431 represent antibody Fc amino acid sequences used in the isolation of the peptides of the invention. The peptides compete for binding ErbB2 with naturally occurring ligands, and may be used to treat disorders characterized by over expression of HER2/ErbB2 such as cancers, diseases of the nervous system, musculature and epithelia, e.g. nervous system metabolic disorders, nutritional deficiency or toxic agents. In particular the synthetic peptide ligands may be used to treat Alzheimer's disease, Parkinson's disease, Parkinson's disease, parkinson's disease, parkinson's disease, parkinson's disease, meniere's disease and neuropathy associated with diabetes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, erbB2; HBR2; cancer; nervous system disease; stroke; ischaemia; metabolic disorder; nutritional deficiency; Alzheimer; s disease; Parkinson's disease; epilepsy; multiple solerosis; Huntington's chorea; Down's syndrome; nerve deafness; Meniere's disease; diabetic neuropathy.
                                                                                                                                                                                                                                                                                                                                                                                 Non-naturally occurring peptide ligands which compete for binding human er32 gene products, useful for treating e.g. Alzheimer's disease, multiple sclerosis and diabetic neuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fusion protein; immunoglobulin; multidimerization domain; ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 PREEQFINSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 PREEQENSTYRVVSVLTVLHQDWINGKRYKCKVSNKGLPSSIEKTISKAK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Match 96.9%; Score 565; DB 4; Length 218; Local Similarity 97.3%; Pred, No. 6.9e-49; les 107; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 2A; 116pp; English
                                                                                                                                                                                                   30-JUN-2000; 2000WO-US018283
                                                                                                                                                                                                                                       99US-0142232P
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                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                               WPI; 2001-123048/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 218 AA;
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                                                                                                                          WO200101748-A2
                                                                                                                                                                                                                                       02-JUL-1999;
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                                                                                          Homo sapiens.
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                                                                                                                                                               11-JAN-2001
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                                                                                                                                                                                                                                                                                                                Dennis MS;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 APPVAGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPBVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 APEFLAGESSYFLEPPKEKDTLMISRIPEVITCVVVDVSQEDPEVQENWYVDGVEVHNAKIK 61
                                                                                                                                                                                                     Novel fusion polypeptides comprising a peptide ligand domain which functions to target hybrid molecule to target cell, and immunoglobulin constant region multimerization domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibody; antigen; immunoglobin; ADCC; CDC; anti-globin response; antibody dependant cell mediated cytotoxicity; complement dependant cytotoxicity; epidermal growth factor receptor; tumour necrosis factor; ymphocyte; tetravalent antibody; cytostatic; antiinflammatory; antipsoriatic; dermatological; antibacteria antianflamatory; antipsoriatic; antinheumatic; antibacterial; antiantmatic; neuroprotective; immunosuppressive; antibacterial; antiallergic; antidiabetic; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Native sequence human 1gG Fc region sequence humIgG4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

96.9%; Score 565; DB 4;
Best Local Similarity 97.3%; Pred. No. 6.9e-49;
Matches 107; Conservative 0; Mismatches 3;
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                                                                                                                                                                       WPI; 2001-123106/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200177342-A1.
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09-JAN-2002; 2002US-0347694P.

(GETH) GENENTECH INC

WPI; 2003-421411/39.

Presta LG;

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This invention relates to an isolated antibody comprising a dimerisation domain and three or more antigen binding sites amino-terminal to the domain. It is cytostatic, antifilammatory, antibacterial, immunosuppressive, antiallergic, an apoptosis inducer, a vaccine and used in gene therapy. Along with a cytotoxic agent, is useful for treating a disorder agent and ammual, for inducing apoptosis of a cancer.

In gene therapy. Along with a cytotoxic agent, is useful for treating a disorder agent and for killing a Dello or a cell which overexpresses or expresses an ErbB receptor and for treating benign and malignant tumours, inflammatory, angiogenic and immunological disorders. Autoimmune the seeptor and for treating benign and malignant tumours, inflammatory, angiogenic and immunological disorders. Autoimmune the useful for immunodiagnosis of various diseases including cancer, for human therapy in redirected cyctotoxicity, and also useful as fibrinolytic agents or vaccine adjuvants, useful as affinity purification agents in adjuvants, useful as affinity purification agents in specific cells, tissue or serum, and useful for blocking an immune specific cells, tissue or serum, and useful for blocking an immune bivalent antibody by a cell expressing an antigen to which the antibodies bind. The antibody by a cell expressing an antigen to which the antibodies bind. The antibody comprises three or four heavy chain variable domains which are able to combine with three or four heavy chain variable domains continue antigen. This sequence represents the native sequence human 1967 the same antigen. This sequence represents the native equence human 1967 the same antigen.
                                                                                  Novel engineered antibody useful in therapeutic applications, contains a dimerization domain and three or more antigen binding sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; antibody; IgG4; cytostatic; immunosuppressive; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APEFLGGSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PREEDFNSTYRVVSVLTVLHQDWLNGKBYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PREEQFINAL TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.9%; Score 565; DB 5; Length 21 97.3%; Pred. No. 6.9e-49; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "given as 'Z' in Fig 23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABR42442 standard; protein; 218 AA
                                                                                                                                                    Disclosure, Fig 3; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-OCT-2002; 2002WO-US033739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-2001; 2001US-0337642P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 97.3
Matches 107; Conservative
Presta LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human IgG4 Fc region.
                                          WPI; 2002-049149/06.
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Misc-difference 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fc region, humlgG4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003035835-A2
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Miller KL,
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The present sequence is the protein sequence of the Fc region of human bout 80-loik of the glycoprotein comprises a glycoprotein having a Fc region. About 80-loik of the glycoprotein comprises a mature core carbohydrate structure which lacks fucose attached to the Fc region. The glycoprotein preferably comprises an antibody, and the Fc region is preferably a human igg Fc region, especially a human igg1, igg2, igg3 or igg4 Fc region. The glycoprotein binds FcgammaRill with better affinity, or mediates antibody elependent cell-mediated cytotoxicity more effectively, than the plycoprotein including fucose. The antibody may be chimeric, humanised or human and binds a B-cell surface marker, an ErbB receptor, a tumourassociated antigen or an angiogenic factor, CD20, HER2, vascular endothelial growth factor, CD40 or prostate stem cell antigen. The composition is useful for treating cancer, autoimmune disease, an inflammatory disorder or infection in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 APEFLGGPSVFLFPPKPKDFLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 61
                                                                                                                                   composition comprising a glycoprotein having a Fc region useful for ating cancer, autoimmune disease, inflammatory disorder or infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 APPVAGGPSVFLFPPKPKDTLMISRTPBVTCVVVDVSQEDPBVQFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heterologous fusion protein related protein sequence SEQ ID NO:19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hyperglycosylated granulocyte-colony stimulating factor; G-CSF; human albumin; human albumin analogue; immunoglobulin; Fc; immunostimulant; protein therapy; neutrophil level; insufficient circulating neutrophil level; chronic congenital neutropenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PREEQFINSTYRVVSVLTVLHQDWINGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.9%; Score 565; DB 6; L
97.3%; Pred. No. 6.9e-49;
tive 0; Mismatches 3;
                                                                                                                                                                                                           Disclosure, Fig 23; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADD32013 standard; protein; 229 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-MAR-2002; 2002US-0361948P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-FEB-2003; 2003WO-US003120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heterologous fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 97.3
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BLIL ) LILLY & CO ELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003076567-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JAN-2004
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                                                                                                                                                                          in a mammal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADD32013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
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The present invention describes a heterologous fusion protein (1)

comprising a hyperglycosylated granulcyte-colony stimulating factor (G-
CSF) analogue fueed to a polypeptide having human albumin, human albumin,
analogues, or fregments of human albumin, or the Fc portion of an immunoglobulin, or
fragments of the Fc portion of an immunoglobulin. Also described: (1) a

heterologous fusion protein, which is the product of the expression in a

controlled caid sequence comprising: (a) polymucleotides encoding (1); or

host cell of an exogenous DNA sequence encoding (1); (2) an isolated

controlled acid sequence comprising: (a) polymucleotides encoding (1); or

(b) a polymucleotide, which comprises any of 15 DNA sequences each

comprising 1044 base pairs (see ADD1996 to ADD12010), fused to the DNA

comprising the administration of (1); (4) pharmaceutical formulations

comprising the administration of (1); (4) pharmaceutical formulations

comprising the administration of (1); (4) pharmaceutical formulations

comprising brotein; (1); (5) a vector comprising the polymucleotide of (2);

(6) host cells comprising the vector of (5), or expressing at least one

comprising protein; and (7) producing (1). (1) has immunostimulant

activity, and can be used in protein therapy. (1) can be used for

increasing neutrophil levels in ammmal. (1) are particularly useful in

controphil levels, or for the manufacture of a medicament for the

createner of patients with insufficient circulating

controlled by stimulation of circulating neutrophils such as after

chemotherapy regimens or in chronic congenital neutrophil action.

chemotherapy regimens or in chronic congenital neutrophils. The present

chemotherapy regimens or in chronic congenital neutrophila. The present

chemotherapy regimens or in chronic congenital neutrophila. The present
                                                                                                             New heterologous fusion proteins with granulocyte-colony stimulating factor activity, useful for increasing neutrophil levels and treating patients with low circulating neutrophils, such as after chemotherapy or
                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 19; 126pp; English,
Kuchibhotla U;
                                                        WPI; 2003-902770/82.
Beals JM,
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1 APPVAGGPSVFLPPPKPKDTIMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60 13 APEPLGGPSVFLPPPKKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 72 0; Gaps 61 PREEOFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110 73 PREEGFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 122 96.9%; Score 565; DB 7; Length 229; 97.3%; Pred. No. 7.3e-49; live 0; Mismatches 3; Indels Best Local Similarity 97.3 Matches 107; Conservative Query Match В à

Sequence 229 AA;

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Human, glucagon-like peptide 1, GLP-1; albumin; immunoglobulin, 1g, therapy; non-insulin diabetes mellitus; obesity; antidiabetic; anorectic; Gly8-Glu22-GLP-1-CEx-linker-Immunoglobulin G4 (1964) fusion protein. AAE30927 standard; protein; 284 AA. (first entry) fusion protein. Homo sapiens. Unidentified. 24-FEB-2003 Chimeric. AAE30927; RESULT 13

WO200246227-A2.

Vaccine, B-cell malignancy; lymphoma; leukaemia; tumour; gene amplification; lmmunotherapy; therapy; immunoglobulin; C-gamma-4;

gene amplification.

W09741244-A1

06-NOV-1997.

96US-00644664. 96US-00761277.

06-DEC-1996; 01-MAY-1996;

(GENI-) GENITOPE CORP.

97WO-US007039.

25-APR-1997;

Immunoglobulin C-gamma-4 region.

11-MAY-1998 (first entry)

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Movel heterologous fusion protein, useful for treating non-insulin dependent diabetes mellitus or obesity, comprises a glucagon-like peptide 1 compound fused to human albumin or to the Fc portion of an
                                                                                                                                                                                                                                                                                                                 The invention relates to a heterologous fusion protein comprising a first polypeptide fused to a second polypeptide, where the polypeptides has a N-terminus and a C-terminus and the first polypeptide is a glucagon -like peptide 1 (GLP-1) compound and the second is a human albumin or its analogue or fragment, where the C-terminus of first polypeptide is fused to the N-terminus of the second polypeptide. The invention is useful for the N-terminus of the second polypeptide. The invention is useful for normalising blood glucose levels in mammal, for treating a patient with medicament for treating the above mentioned diseases. The present sequence is GLP-1 fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 APBFLGGPSVFLFPPREXEXOTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVFNAKTK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 APPVAGGPSVFLFPPKEKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PRESQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 PREBQENSTYRVVSVLTVIHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

96.9%; Score 565; DB 6; Length 28
Best Local Similarity 97.3%; Pred. No. 9.5e-49;
Matches 107; Conservative 0; Mismatches 3; Indels
                                                                                                                                            Tschang SR;
                                                                                                                                                                                                                                                                                       Example 6; Page 83; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW37346 standard; protein; 327 AA
                                              29-NOV-2001; 2001WO-US043165.
                                                                              07-DEC-2000; 2000US-0251954P.
                                                                                                                                            Glaesner W, Micanovic R,
                                                                                                             (BLIL ) LILLY & CO BLI
                                                                                                                                                                            WPI; 2003-018534/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 284 AA;
                                                                                                                                                                                                                                                           immunoglobulin.
                 13-JUN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW37346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
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invention provides a method for the production of tumour-specific 1gd derived from a B-cell lymphoma patient. In the novel method, expression plasmids containing the patient's VH region(s) joined to either a C-gamma-3 (see AAPT91188) or C-gamma-4 (see AAT97189) sequence and expression plasmids containing the patient's VL region(s) joined to either a C-kappa plasmids containing the patient's VL region(s) joined to either a C-kappa along with a selectable and amplifiable marker into a cell line (e.g. BW5147.G.1.4), and transfected cells are then subjected to selection and amplification. The method permits the production of a multivalent vaccine which reflects the degree of somatic variation found within the patient's tumour. These novel multivalent vaccines provide superior vaccines for treatment of B-cell lymphoma
                                                                                                                                         Multivalent vaccine to treat B cell lymphoma or leukaemia - comprises at least 2 different recombinant variable regions of immunoglobulin molecules derived from B cell lymphoma cells.
                                                                                                                                                                                                                                                                                           This protein comprises an immunoglobulin (Ig) C-gamma-4 region.
                                                                                                                                                                                                                                          Example 10; Page 126-127; 177pp; English.
                                                                      WPI; 1997-549743/50.
                                                                                             N-PSDB; AAT97189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 327 AA;
                       Denney DW;
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1 APPVAGGPSVFLFPPKPKDTLMISRTPEVICVVVDVSQEDPEVQFNWYVDGVEVHNAKIK Gaps .. o 96.9%; Score 565; DB 2; Length 327; ilarity 97.3%; Pred. No. 1.1e-48; Conservative 0; Mismatches 3; Indels 3; Indels Query Match Best Local Similarity Matches 107; Conserv

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8 용 AAM47859 standard; protein; 327 AA

AAM47859;

(first entry) 22-FEB-2002 Human Ig-G4 heavy chain constant region amino acid sequence.

Human; immunoadhesin; intercellular adhesion molecule; ICAM-1; human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold; transgenic plant

Homo sapiens

WO200183529-A2

. L002-VCN-80

28-APR-2001; 2001WO-US013932

28-APR-2000; 2000US-0200298P

(PLAN-) PLANET BIOTECHNOLOGY INC.

Larrick JW, Wycoff KL;

2002-041481/05

WPI; 2002-041481/ N-PSDB; ABA05268.

Immunoadhesin for treating human rhinovirus infection comprises chimeric

The invention relates to an immunoadhesin comprising: (a) a chimeric intercellular adhesion molecule (ICAM)-1 comprising a rhinovirus receptor protein linked to at least a portion of an immunoglobulin heavy chain; and (b) optionally a J chain and secretory component associated with the cand (b) optionally a J chain and secretory component associated with the chimeric ICAM-1 molecule. The immunoadhesin is useful for glycosylation and virucide activity. The immunoadhesin is useful for reducing infection by human rhinovirus (RRV) and hence the initiation or spread of the common cold by HRV. The immunoadhesin binds to HRV and reduces its infectivity, competing with cells surface ICAM-1 for binding sites, interfering with virus entry or uncoating and directing premature clease of viral RNA and formation of empty capsids. Expression of the immunoadhesin having multiple binding sites have a higher effective immunoadhesin having multiple binding sites have a higher effective immunoadhesin. Association of secretory component and immunoglobulin J chain increases the stability of the immunoadhesin in the wuccosal conformment. Production is significantly less expensive in plants than in animal cell culture and production in plants is safer for human use, since plants are not known to harbor any animal viruses. The present conformed is that of a human immunoglobulin protein sequence, useful to intercellular adhesion molecule-1, and optionally a J chain and secretory Disclosure; Fig 7, 138pp; English. component in association.

Sequence 327 AA;

Gaps ó Length 327; Indels 96.9%; Score 565; DB 5; 97.3%; Pred. No. 1.1e-48; ive 0; Mismatches 3 Best Local Similarity 97.3 Matches 107; Conservative Query Match

1 APPVAGGPSVFLFPPKPKDTLMISRTPRVTCVVVDVSQBDPEVQFNWYVDGVEVHNAKTK 60

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111 APEFLGGPSVFLFPPFKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVFNAKTK 170 61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110 셤 ò

Search completed: April 29, 2004, 08:44:23 Job time : 52.5 secs

us-09-674-857-3.rag

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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protein search, using sw model OM protein April 29, 2004, 08:37:12 ; Search time 50.5 Seconds Run on:

(without alignments) 615.450 Million cell updates/sec

US-09-674-857-3 ritle:

1 APPVAGGPSVFLFPPKPKDT......CKVSNKGLPSSIEKTISKAK 110 score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Fotal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_29Jan04:* 1: genesern1000. geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp1990s: + geneseqp2000s:*geneseqp2001s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

		Description		6 Mutate	09010	Aay97175 Human FGF	4 Human		MoTAbi	4 Human	Aae35231 Human imm	Abb81492 Human mut	Abb81491 Human mut		Aay05688 Modified		Aab07541 Amino aci	8 Human	σ	Abb81493 Ztnfr12-t	Aae35228 Human TAC	Human.	5 Human	6 Human	Aae35223 Human TAC	Abb81645 Zcytor19	Aau76912 Human CRF
SUMMARIES		A	AAY54998	AAY54996	AAW85689	AAY97175	AAY97174	AAY97173	AAW85692	AAE33524	AAE35231	ABB81492	ABB81491	AAE35220	AAY05688	AAW97756	AAB07541	AAE35218	AAE35219	ABB81493	AAE35228	AAE35224	AAE35225	AAE35226	AAE35223	ABB81645	AAU76912
		8	m	m	7	m	m	m	N	9	9	មា	ហ	v	Ŋ	(7)	m	9	Q	Ŋ	v	φ	v	9	w	Ŋ	'n
		Length	110	109	46B	488	497	525	711	447	251	232	232	250	251	251	251	251	251	328	332	344	348	357	392	473	476
	Query	Match	98.1	97.2	95.7	95.7	95.7	95.7	95.7	92.6	95.4	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1
		Score	576		vo	φ	562	vo	ø	vo	o	ഗ	S	ß	വ	വ	S	വ	ഹ	വ	ഹ	ഗ	ഹ	S	LO.	S	S.
	Result	No.	П	7	m	47*	ហ	9	7	80	6	10	턴턴	132	13	14	15	16	17	8	19	20	21	22	23	24	25

Humai	Aau76916 Human 2cy	Humar	Aae29073 Human IL-	Aab85286 IL-20RA-I	Abg67217 IL-20RA e	_	-		Aau04062 Human IL-	Abg67205 IL-20RA e	Aae23358 Human IL-	Abb05743 Human zcy	Add68180 Human zcy	_	Aar41684 Undefined	Aay42621 Human IgG	Aar87023 Immunoglo	Aaw02305 Human IgG	Aar97264 Human imm
AAE30845	AAU76916	AAE30844	AAE29073	AAB85286	ABG67217	AAE23361	AAB29072	AAB85274	AAU04062	ABG67205	AAE23358	ABB05743	ADD68180	AAR27680	AAR41684	AAY42621	AAR87023	AAW02305	AAR97264
ø	Ŋ	ø	w	4	'n	ហ	Ŋ	4	4	Ŋ	'n	'n	7	~	~	~	N	~	N
476	484	484	556	559	559	559	573	594	594	594	594	764	764	110	110	116	212	212	212
95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	94.9	94.9	94.9	94.9	94.9	94.9
558	558	558	558	558	558	558	558	558	558	558	558	558	558	557	557	557	557	557	557
56	2.1	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4.5

ALIGNMENTS

RESULT 1

AAYS4998 standard; protein; 110 AA Mutated CH2 sequence Gideltaac. (first entry) 17-FEB-2000 AAY54998; AAY54998

Synthetic.

W09958572-A1

18-NOV-1999.

99WO-GB001441. 07-MAY-1999; (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

98GB-00009951.

08-MAY-1998;

Williamson LM; Clark MR, Armour KL,

WPI; 2000-039075/03.

Immunoglobulic-derived binding molecules that do not activate complement or trigger cytotoxic activities and maintaining desirable immunoglobulin properties.

Claim 12, Fig 17, 81pp, English.

This sequence represents the mutated CH2 molecule Gideltaac, and is a binding molecule of the invention. The recombinant binding molecule is capable of binding a target molecule without triggering complement dependent lysis, or the cell-mediated destruction of the target comprises: [a] a binding domain capable of binding a target molecule; and (b) an effector domain that is homologous to all or part of a constant

Claim 12, Fig 17; 81pp; English.

properties.

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compain of a human immunoglobulin G (IgG) heavy chain. The binding molecule is used to bind a target molecule (especially FogammaRID causing inhibition of B cell activation, mast cell degranulation or phagocytosis). The binding molecule can be used to prevent or inhibit the binding molecule can be used to prevent or inhibit the binding molecule is useful for the transplant or incompanies, organ transplant rejection, bone-marrow transplant rejection, bone-marrow transplant rejection, bone-marrow transplant rejection, bone-marrow transplant or rejection, autoimmunity (e.g. vasculitis, autoimmunity (e.g. vasculitis, autoimmunity (e.g. vasculitis, autoimmunity (e.g. cotornaty incompanies) (cotornaty incompanies) (cotornaty incompanies) (cotornaty artery occlusion). The binding molecules do not activate coronary artery occlusion). The binding molecules do not activate complement or trigger cycotoxic activities through FogammaR and desirable companienty. Further, they still bind Protein A, which is consistent with being able to cross the human placenta through interaction with FCRn (neonatal FC receptor)
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Sequence 110 AA;

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9
                                                                                                                                      1 APPVAGGPSVFLFPPKFKDTLMISRIPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                       1 APPVAGGPSVFLFPPKKPKDTLAISRTPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKIK
                                              0; Gaps
                                                                                                                                                                                                            PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                    61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
Length 110;
Score 576; DB 3;
Pred. No. 9.3e-52;
Query Match
98.1%; Score 576; DB
Best Local Similarity 99.1%; Pred. No. 9.3e
Matches 109; Conservative 0; Mismatches
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AAY54996 standard, protein, 109 AA. Mutated CH2 sequence Gldeltaab. (first entry) 17-FEB-2000 AAY54996;

Binding molecule; CH2 sequence; complement dependent lysis; FegammaRIID; cell-mediated destruction; human; immunoglobulin G; IgG heavy chain; B cell activation; mast cell degranulation; phagocycosis; vasculitis; Crohn's disease; graft-vs-host disease; organ transplant rejection; bone-marrow transplant rejection; autoimmune disease; asthma; allergy; alloimmune thrombocytopaenia; arthritis; erythroblastosis focealis; neonateal alloimmune thrombocytopaenia; decodesis focealis; sickle cell anaemia; coronary artery occlusion.

WO9958572-A1.

Antibody, humanised, variable region, heavy chain; light chain; interferon gamma, IFN; treatment; prevention; septic shock; cachexia; immune disease; multiple sclerosis; Crohn's disease; skin disorders; inflammation; neoplasia; dermatitis; monoclonal antibody; diabody; scFv;

multivalent; ruminant

Mus musculus.

Peptide

Domain Somain

Synthetic

D9D10 heavy chain fusion protein.

(first entry)

12-AUG-1999

137
 note= "Humanised heavy chain variable domain of D9D10"

. .20 note= "D9D10 light chain signal peptide"

Location/Qualifiers

'note= "Human IgG1 heavy chain constant domain"

.467

Misc-difference

note= "Leu added by cloning strategy"

18-NOV-1999.

(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

98GB-00009951.

08-MAY-1998;

Williamson LM; Clark MR, Armour KL,

WPI; 2000-039075/03.

Immunoglobulic-derived binding molecules that do not activate complement or trigger cytotoxic activities and maintaining desirable immunoglobulin

```
This sequence represents the mutated CH2 molecule Gldeltaab, and is a binding molecule of the invention. The recombinant binding molecule is capable of binding a target molecule without triggering complement dependent lysis, or the cell-mediated destruction of the target complement capable of binding a target molecule; and comprises: (a) a binding domain capable of binding a target molecule; and compain of a human immunoglobulin G [IgG) heavy chain. The binding constant domain of a human immunoglobulin G [IgG) heavy chain. The binding constant constant constant binding inhibition of B cell activation, mast cell degranulation or phagocytosis). The binding molecule can be used to prevent or inhibit the binding molecule can be used to prevent or inhibit the binding molecule is useful for the trarget constant transplant rejection, bene-marrow transplant rejection, autoimmunity (e.g. vasculitis; constant alloimmunity (e.g. vasculitis), alloimmunity (e.g. vasculitis; constant and allergy), chronic or acute inflammatory diseases (e.g. Crohn's, HDN chronic or acute inflammatory diseases (e.g. Crohn's, HDN condary artery occlusion). The binding molecules do not activate complement or trigger cytotoxic activities through FcgammaR and desirable cornary artery occlusion). The binding molecules do not activate complement or trigger cytotoxic activities through FcgammaR and desirable cornary and are therefore likely to have reduced immunogenicity. Purther, they still bind Protein A, which is consistent contant all be to cross the human placenta through interaction with FcRn (near all purch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 APPVA-GPSVFLFPPKPKDTIMISKTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PREEQYNSTYRVVSVITVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PREEDYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.2%; Score 570.5; DB 3; Length 109; 99.1%; Pred. No. 3.4e-51; ive 0; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW85689 standard; protein; 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (neonatal Fc receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW85689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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New antibodies which bind and neutralise interferon-gamma (IFN gamma) can be used as a medicant, for preventing or treating septic shock, cachexia, immune diseases including multiple sclerosis and Crohn's disease and skin disorders including bullous, inflammatory and neoplastic dermatoses. The antibody is selected from a single chain antibody of chimaria cartibody comprising the humanised variable domain of the monoclonal mouse anti-IPN gamma antibody DBD10; a multivalent antibody.

Or a ruminant antibody. The antibodies are also useful for determining or a ruminant antibody comprised of the humanised DBD10 and the mouse DBD10 and constructed. The light chain comprised cDNA encoding the mouse DBD10 constructed. The light chain comprised cDNA encoding the mouse DBD10 constructed. The light chain comprised cDNA encoding the mouse DBD10 light chain and a human immosplobulin kappa light chain constant region. The heavy chain constant constant region. The heavy chain constant constant region. The heavy chain constant chain constant completed cDNA encoding the mouse DBD10 light chain leader sequence tollowed by the humanised DBD10 light chain leader sequence. This comprised cDNA encoding the mouse DBD10 light chain leader sequence tollowed by the humanised DBD10 light chain leader sequence. This case then mutated. Four overlapping synthetic oligonuclectides (AxX08599) to generate PCR-V fragment. The humanised heavy chain variable domain was then subsequently amplified using two primers (AxX08594) and then cloned into pGEM-T-th two primers (AxX08593). AxX08599, and cloned tinto pGEM-T to give pGEM-T-the humanised heavy chain constant domain was complified with two primers (AxX08599). AxX08599, and cloned tinto pGEM-T to give pGEM-T-the humanised beavy chain constant domain was permitted by the pGEM-T-the proposer the proposer and plications were then performed to generate PCR-VIII fragment and AxX08599, AxX08599, and cloned the resulting PCR-X fragment inserted into pGEM-T-the a description of the constant constant de
                                                                                                                                                                                                                                                                                                                                                                                  New engineered antibodies which bind and neutralise interferon-gamma useful for prevention and treatment of septic shock, cachexia, immune diseases and skin disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fusion cDNA see GENESEQ records AAX08573-X08584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 9; 134pp; English.
                                                                                                               98WO-EP005165.
                                                                                                                                                         97EP-00870122.
98EP-00870139.
                                                                                                                                                                                                                              (INNO-) INNOGENETICS NV
                                                                                                                                                                                                                                                                                                                         WPI; 1999-180969/15,
N-PSDB; AAX08631.
                                                                                                                                                                                                                                                                             Buyse M, Sablon E;
                                                                                                               14-AUG-1998;
                                                                                                                                                              18-AUG-1997;
                                                                                                                                                                                    18-JUN-1998;
                      WO9909055-A2
                                                                  25-FEB-1999.
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95.7%; Best Local Similarity 95.5 Matches 105; Conservative Query Match Best Local Similarity Sequence 468 AA;

ò 임 ò 임

1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHBDPEVKFNWYVDGVEVHNAKTK 60 Gaps ö 3; Indels Score 562; DB 2; Pred. No. 1.5e-49; 2; Mismatches 3;

251

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FGF-R; fibroblast growth factor receptor; extracellular domain; 1961; immunoglobulin; G1; oligomerization domain; Fc region; fusion protein; inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnerary; ophthalmological; anti-proliferative.
                                                                                                                                                                                                                                                              /note= "This mutation decreases the affinity of the Fc portion for Fc receptors"
                                                                                                                                                                                                                                                                                         /label= P376S
/note= "This mutation decreases the affinity of the Fc
portion for complement"
                                                                                                                                                                                                                                label= Human_IgGl_Fc_region
'note= "Contains hinge region and domains CH2 and CH3"
                                                                                                                                                           22. 257
/label= FGF-R1_extracellular_domain
/note= "The Ig I segment and acid box are deleted"
                                                        Human FGF-RI Extracellular domain-Ig Fc fusion protein 6.
                                                                                                                                              . .21
|abel= FGF-R1_signal_peptide
                                                                                                                                                                                                     57. .222 _____
|abel=_Ig_III_segment
                                                                                                                                                                                           label Ig II segment
                                                                                                                                    socation/Qualifiers
         AAY97175 standard; protein; 488 AA.
                                                                                                                                                                                                                                                         label= L276E
                                        (first entry)
                                                                                                                                                                                                                        .488
                                                                                                                                                                                                                                                                                   Misc-difference 376
                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                      Homo sapiens
                                         04-DEC-2000
                         AAY97175;
                                                                                                                                             Peptide
                                                                                                                                                               Domain
                                                                                                                                                                                        Domain
                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                         Region
AAY97175
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WO200046380-A2.

10-AUG-2000.

07-FEB-2000; 2000WO-US003166.

99US-0119002P. 08-FEB-1999;

(CHIR) CHIRON CORP.

Kavanaugh WM, Ballinger M;

WPI; 2000-514961/46. N-PSDB; AAAS2132.

New polypeptide comprising a fibroblast growth factor receptor extracellular domain fused to a heterologous oligomerization domain for treating FGF-, angiogenesis-, or FGF receptor-mediated disorders.

Claim 14; Page 68-69; 70pp; English

Novel fusion protein constructs comprise a fibroblast growth factor (FGF) receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin (FGF) lacking the immunoglobulin (FGF) lacking the immunoglobulin (FGF) are region, CHI, CH2, CH3 or CH4 region, or light chain of an immunoglobulin molecule, or a peptide with a lacting for more rigper motif. The Ig I segment is not necessary for binding of acidic FGF and basic FGF (bFGF). The Ig I deletion further increases the affinity for aFGF and heparin, protects the core of the molecule from protecting and abrogates the heparin requirement for aFGF binding. The new fusion polypeptides are better FGF inhibitors than FGF monomer proteins. The FGFR-IG FC fusion dimers are active as FGF antagonists at pubraneonal roncentrations and were 20-fold more potent than the FGF-R monomer protein as competitors of bFGF binding to immobilized FGF-R monomer grotein as competitors of bFGF binding to immobilized FGF-R.

RESULT

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N-PSDB; AAA52131.
                                                                                                                                                                                                                                                                                Sequence 497 AA;
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                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                        272 APELEGGESVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 331
                                                                                                             9
mediated disorders, such as tumourigenesis (e.g. bladder, breast, lung, rectal, testis and cervical tumours), neovascularization (e.g. diabetic retinopathy, neovascular glaucoma, wound healing and corneal scarring) and hyper-proliferation of vascular smooth muscle cells (e.g. postangioplasty and postatherectomy restenosis)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    866. .497
|Jabel= Human IgG1 Fc region
|mote= "Contains hinge region and domains CH2 and CH3"
                                                                                                                                                                                                                                                                                       FGF-R; fibroblast growth factor receptor; extracellular domain; IgGl; immunoglobulin; Gl; Oligomerization domain; Fc region; fusion protein; inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnerary; ophthalmological; anti-proliferative.
                                                                                                             1 APPVAGGPSVFLFPPKPKDTLMISRTPRVTCVVVDVSHBDPRVKFNWYVDGVBVHNAKTK
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= L285B
/note= "This mutation decreases the affinity of the
portion for Fc receptors"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "This mutation decreases the affinity of the
                                                                                                                                                                                                                                                                                                                                                                                    22. .257
/label= FGF-R1_extracellular_domain
/note= "The Ig I segment and acid box are deleted"
                                                                                                                                                 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                           332 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK 381
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                                                                       Score 562, DB 3; Length 488;
Pred. No. 1.6e-49;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                       Human FGF-RI Extracellular domain-Ig Fc fusion protein 5.
                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. 21
/label= FGF-R1_signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 portion for complement'
                                                                                                                                                                                                                                                                                                                                                                                                                                57. .222 ___label=_Ig_III_segment
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/label=_Ig_II_segment
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                                                                                                                                                                                                                  AAY97174 standard; protein; 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= P385S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0119002P
                                                                         95.7%;
95.5%;
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                                                                                                                                                                                                                                                       (first entry)
                                                                                             Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORP.
                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                         Sequence 438 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHIR ) CHIRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200046380-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kavanaugh WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-FEB-1999;
                                                                                                                                                                                                                                                      04-DEC-2000
                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                     AAY97174;
                                                                                                                                                   61
                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
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Novel fusion protein constructs comprise a fibroblast growth factor (FGF) receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin (1g) I segment fused to a heterologous oligomerization domain that comprises an immunoglobulin Fc region, hinge region, CH1, CH2, CH3 or CH4 cregion, or light chain of an immunoglobulin molecule, or a peptide with a leucine zipper motif. The Ig I segment is not necessary for binding of acidic FGF and heparin, protects the core of the molecule from proteolysis, and abrogates the heparin requirement for aFGF binding. The caffinity for aFGF and heparin, protects the core of the molecule from proteins. The FGFR-IG FC fusion diamers are active as FGF antagonists at concernations and were 20-fold more potent than the FGF-R subnanomolar concentrations and were 20-fold more potent than the FGF-R chain on constructs are useful to treat FGF, angiogenesis, or FGF-R. Chainon constructs are useful to treat FGF-, angiogenesis, or FGF-R chained disorders, such as tumourigenesis (e.g. bladder, breast, lung, rectal, testis and cervical tumours), neovascularization (e.g. diabetic relingantly, neovascular glaucoma, wound healing and corneal scarring) and hyper-proliferation of vascular smooth muscle cells (e.g. cornegisting)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 APPVAGGESVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                               New polypeptide comprising a fibroblast growth factor receptor extracellular domain fused to a heterologous oligomerization domain for treating FGP-, angiogenesis-, or FGF receptor-mediated disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FGF-R; fibroblast growth factor receptor; extracellular domain; IgG1; immunoglobulin; G1; oligomerization domain; Fc region; fusion protein; inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnerary; ophthalmological; anti-proliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341 PREEGYNSTYRVVSVLTVLAQDALNGKEYKCKVSNKALPASIEKTISKAK 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human FGF-RI Extracellular domain-1g Fc fusion protein 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 562; DB 3; Length 49
Pred. No. 1.6e-49;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22. .285
/label= FGF-R1 extracellular domain
/note= "1g I segment is deleted"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .21
/label= FGF-R1_signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Acid_box_segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87. .139
/label= Ig_II_segment
286. .293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                             Claim 14; Page 65-66; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY97173 standard; protein; 525 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 95.5
Matches 105; Conservative
WPI; 2000-514961/46
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Antibody; humanised; variable region; heavy chain; light chain; interferon gamma; IFW; treatment; prevention; septic shock; cachexia; immune disease; multiple sclerosis; Crohn's disease; skin disorders; inflammation; neoplasia; dermatitis; monoclonal antibody; diabody; scFv; multivalent; ruminant.

note= "Humanised heavy chain variable domain of D9D10"

...20 |abel= Mouse_D9D10_light_chain_signal_peptide

Location/Qualifiers

Synthetic.

Peptide

Domain Domain

'note= "Human 1gG1 heavy chain constant domain"

.467 137

Misc-difference 468

Region

note= "Leu added by cloning strategy"

473. .711 /label= Humanised)_D9D10_ScFv 469. .472 /label= Gly(3)Ser_linker

WO9909055-A2

25-FEB-1999

14-AUG-1998; 18-AUG-1997; 18-JUN-1998;

97EP-00870122. 98EP-00870139. 98WO-EP005165

(INNO-) INNOGENETICS

Sablon E;

Buyse M,

WPI; 1999-180969/15.

N-PSDB; AAW85692

AAW85692 standard; protein; 711 AA.

(first entry)

12-AUG-1999

MoTAbII fusion protein

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Novel fusion protein constructs comprise a fibroblast growth factor (FGF) receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin coeptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin that comprises an immunoglobulin Fc region, hinge region, CHI, CH2, CH3 or CH4 region, or light chain of an immunoglobulin molecule, or a peptide with a redicin FGF and basic FGF (FGF). The Ig I segment is not necessary for binding of a cidic FGF and basic FGF (FGF). The Ig I deletion further increases the affinity for a FGF and heparin, protects the core of the molecule from proteolysis, and abrogates the heparin requirement for aFGF binding. The cast in FGF-R inhibitors than FGF-R monomer proteins. The FGFR-IG FC fusion dimers are active as FGF antagonists at subnanomolar concentrations and were 20-fold more potent than the FGF-R funion constructs are useful to treat FGF-, angiogenesis-, or FGF-R. Chusion constructs and carvial tumours), neovascularization (e.g. diabetic retinopathy, neovascular glaucoma, wound healing and corneal scarring) and hyper-proliferation of vascular smooth muscle cells (e.g. postangioplasty and postatherectomy restenosis)
                                                                                                                                                                         Ę,
                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide comprising a fibroblast growth factor receptor extracellular domain fused to a heterologous oligomerization domain treating FGF-, angiogenesis-, or FGF receptor-mediated disorders.
                                                                                                                                                      /label= P409S
/note= "The mutation decreases the affinity of the
portion for complement"
                                                                                                     ŏ
                  294. .525
/label= Ruman IgG1 Fc region
/Ance= "Contains hinge region and domains CH2
                                                                                    /label= 1313E
/note= "The mutation decreases the affinity
portion for Fc receptors"
                                                                                                                                                                                                               445. .250
/label= Ig_III_segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 14; Page 61-62; 70pp; English
 label= Linker
                                                                                                                                                                                                                                                                                                                                        07-FEB-2000; 2000WO-US003166.
                                                                                                                                                                                                                                                                                                                                                                            99US-0119002P
                                                                                                                                                                                                                                                                                                                                                                                                                                               Kavanaugh WM, Ballinger M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-514961/46.
                                                                                                                                                                                                                                                                                                                                                                                                            (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 525 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAA52130.
                                                                       Misc-difference
                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                    WO200046380-A2
                                                                                                                                                                                                                                                                                                                                                                            08-FEB-1999;
                                                                                                                                                                                                                                                                                                      10-AUG-2000
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                      Region
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New antibodies which bind and neutralise interferon-gamma (IFN gamma) can be used as a medicant, for preventing or treating septic shock, cachexia, immune diseases including multiple sclerosis and Crohn's disease and skin disorders including bullous, inflammatory and neophastic dermatoses. The antibody is selected from a single chain antibody (scFv), a chimeric monoclonal mouse anti-IFN gamma antibody 19910; a multivalent antibody; or a now antibody. The antibodies are also useful for determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 APELLGGFSVFLFPPKFKDTLÆISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHRAKTK 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PREEQYNSTYRVVSVLTVLEQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 562; DB 2; L4 Pred. No. 2.5e-49; 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FN gamma levels in a sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 95.5
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 711 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PREBQYNSTYRVVSVLTVLHQDWLNGKBYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.7%; Score 562; DB 3; Length 525; 95.5%; Pred, No. 1.8e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity Matches 105; Conser

369

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RESULT 7

New engineered antibodies which bind and neutralise interferon-gamma useful for prevention and treatment of septic shock, cachexia, immune diseases and skin disorders.

Disclosure, Fig 20; 134pp; English.

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Length 711; Indels

Sequence 447 AA;

313 PREEGYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK 360

AAE33524 standard; protein; 447 AA

AAE33524;

02-APR-2003

(first entry)

Human AQC2 heavy chain mutant protein, hsAQC2.

Human; very late activation antigen; VLA-1; betal containing integrin; munucological disorder; inflammacory disorder; skin related condition; psoriasis; eczema; burn; dermatitis; respiratory distress syndrome; fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis; fever, migraine headache; inflammatory bowel disease; forthn's disease; irritable bowel syndrome; colitis; colorectal cancer; vascular disease; atherosclerosis; thyroiditis; aplastic anaemia; periarteritis nodosa; agstrifis; FodgKin's disease; rheumatic fever; autoimnume disease; systemic lupus erythematosus; multiple sclerosis; rheumatoid architis; systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome; prand failure; asrcoidosis; Behcet's syndrome; gingivitis; polymyositis; hypersensitivity; graft rejection; transplant rejection; conjunctivitis; graft versus host disease; myocardial ischaemia; mutant; mutein.

Ношо

W0200283854-A2

24-OCT-2002.

12-APR-2002; 2002WO-US011521,

13-APR-2001; 2001US-0283794P. 06-JUL-2001; 2001US-0303689P.

(BIOJ) BIOGEN INC.

Saldanha JW, Karpusas M; Garber EA, Lyne PD,

WPI; 2003-093009/08

New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-mediated immunological or inflammatory disorders, e.g. psoriasis, eczema, burns, dermatitis, and abnormal proliferation of hair follicle cells or fibrosis.

Example 23; Page 92; 248pp; English.

The present invention relates to novel antibodies that specifically bind to very late activation (VLA-1; betal containing integrins) antigens and methods of using these antibodies to treat immunological disorders. The methods of using these antibodies to treat immunological disorders. The mediated immunological or inflammatory disorders such as skin related conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal proliferation of hair follicle cells), fibrosis (e.g. kidney or lung fibrosis), allergic rhinitis, respiratory distress syndrome, asthma, conditis, tendonlitis, respiratory bowel disease, Crohn's disease, destricts, irritable bowel syndrome, collits and colorectal cancer), vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia, or periatreritis nodosa, Hodgkin's disease, myasthenia gravis, rheumatoid autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid arthitis, systemic lupus erythematosus and multiple sclerosis); real failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis, polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or immediate hypersensitivity), graft and transplant rejections, graft verses host disease, conjunctivitis, swelling occurring after injury, myocardial ischaemia or endotoxin shock syndrome. The present sequence is human AQC2 heavy chain mutant protein, heAQC2

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                                                                                                                                  232 APEAAGGPSVPLPPPKPKOTLMISRTPBVTCVVVDVSHBDPBVKFNWYVDGVBVHNAKTK 291
                                                                                        1 APPVAGGPSVFLFPPKPYDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                              Gaps
                                                                                                                                                                                 61 PREBOYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                          292 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 341
  Length 447;
                                            4; Indels
95.6%; Score 561; DB 6; larity 95.5%; Pred. No. 1.8e-49; Conservative 1; Mismatches 4;
                 Local Similarity
es 105; Conserv
  Query Match
                           Best Loca
Matches
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AAE35231 standard; protein; 251 AA AAE35231

RESULT

AAE35231;

(first entry) 28-MAY-2003

Human immunoglobulin gammal mutant protein, Al34S.

Transmembrane activator; calcium modulator; nephrotropic; antibacterial; TACI; tumnour necrosis factor-like protein; ZTNE2; TNF4; immunoglobulin; anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive; glomerulonephritis; asthma; bronchitis; graft rejection; septic shock; demarcological; neuroprotective; cytolophilin ligand-interactor; human; autoimmune disease; systemic lupus erythematosus; multiple sclerosis; diabetes mellitus; rheumatoid arthritis; renal disease; inflammation; mutant; mutein.

Homo sapiens

/note= "FcgammaRI binding site" Location/Qualifiers Binding-site

/note= "Wild-type Ala is replaced with Ser" Misc-difference

WO200294852-A2.

28-NOV-2002,

20-MAY-2002; 2002WO-US015910.

24-MAY-2001; 2001US-0293343P.

(ZYMO) ZYMOGENETICS INC.

Rixon MM,

WPI; 2003-148455/14.

Transmembrane activator and calcium modulator and cyclophilin ligand-interactor (TACI)-immunoglobulin fusion protein, for treating cancer or diabetes, comprises a TACI receptor group and an immunoglobulin group.

Example 1; Col; 71pp; English.

The invention relates to fusion proteins comprising transmembrane activator and calcium modulator and cyclophilin ligand-interactor (TACI) receptor group that binds tumour necrosis factor-like protein (ZTNF) or ZTNF4; and an immunoglobulin group comprising a constant region of immunoglobulin. The invention is used to manufacture a medicament for inhibiting the proliferation of tumour cells in a marmalian subject. The composition comprising the fusion protein may also be used in treating autoimmune diseases (e.g. systemic lupus erythematosus, multiple sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal

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diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft rejection, anaemia and septic shock. The fusion proteins are also used in gene therapy. The present sequence is human immunoglobulin gammal mutant protein. This sequence is used in the exemplification of the invention. Once: This sequence is not shown in the specification, however it is constructed based on human immunoglobulin gammal protein (SEQ ID NO:6) sequence shown in column 92-93 (AAE35214)
                                                                                                                                                                                                                                                                   1 APPVAGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                        35 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWFVDGVEVHNAKTK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ruman, Ztnfr12; tumour necrosis factor receptor; cytostatic; immunosuppressive; dermatological; antiniflammatory; antidabetic; neuroprotective; antinteumatic; antiarthritic; antiasthmatic; nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour; autoimmune disorder; systemic lupus erythematosis: myasthenia gravis; multiple sclerosis; insulin dependent diabetes mellitus; asthenia gravis; rhematoid arthritis; bronchitis; emphysema; renal disease; lymphoma; glomerulonephritis; bronchitis; chronic lymphoid leukaemia; nephritis; pyelonephritis; renal neoplasm; multiple myeloma; myaloidosis; graft-versus host disease; graft rejection; Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a human tumour necrosis factor receptor
                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated human tumor necrosis factor receptor polypeptide, te
Etnfr 12, useful for treating autoimmune disorders, emphysema, end
renal failure or renal disease and lymphoma.
                                                                                                                                                                                                                                                                                                                                               61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                  95 PREEQYNSTYRVVSVLTVIHQDWLNGKEYKCKVSNKALPSPIEKTISKAK 144
                                                                                                                                                                                    Score 560; DB 6; Length 251;
Pred. No. 1.1e-49;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human mutated Fc protein designated Fc5 SEQ ID NO:32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grant FJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB81492 standard; protein; 232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-NOV-2000; 2000US-0246449P.
20-DEC-2000; 2000US-0257131P.
28-UUX-2001; 2001US-031715P.
29-AUG-2001; 2001US-0315565P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-NOV-2001; 2001WO-US047018.
                                                                                                                                                                                        tch 95.4%; al Similarity 95.5%; 105; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-508212/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABN89447.
                                                                                                                                                       Sequence 251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200238766-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-SBP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB81492;
                                                                                                                                                                                          Query Match
Best Local 8
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                                                                                                                                                                                                                               Matches
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designated Ztnfr12 [1]. (I) has cytostatic, immunosuppressive, dermaced Ztnfr12 antiinflammatory, neuroprotective, antidiabetic, antirheumatic, antianthitic, antianthitic, nephrotropic and hypotensive activities, and can be used in gene therapy. (I) can be used for inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12 (e.g. ZTNF4), for treating disorders and disease associated with B lymphocytes or resting B lymphocytes, and for inhibiting the proliferation of tumour cells; [1] is useful for treating autoimmune disorders such as systemic lupus erythematosus, myasthenia gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma, theurachid arthritis, bronchitis, emphysema and end stage renal failure or renal disease such as glomerulomephritis, vasculitis, chronic lymphoid leukaemia, nephritis, and pyelonephritis, wasculitis, chronic lymphoid leukaemia, nultiple myelomas, lymphomas, light chain neuropathy, or amyloidosis, hypertension, large vessel diseases, graft rejection and Crohn's disease, [1] is useful for modulating the immune system, for regulating as cell responses and development, for modulating development of other cells, antibody production and cytokine production, and for modulating T and B cell communication. Human Zinfr11 is located to chromosome 22q13.2. The present sequence represents a mutated For protein designated FCS, which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 APEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; Ztnfr12; tumour necrosis factor receptor; cytostatic; immunosuppressive; dermatological; antinilammatory; antidiabetic; neuvoprotective; antirheumatic; antiarthritic; antiasthmatic; nephrotropic; hypotemsive; qene therapy; B lymphocyte; tumour; autoimmune disorder; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; insulin dependent diabetes mellitus; asthma; rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma; glomerulonephritis; renal neoplasm; multiple myelome; mynyloidosis; personchitis; multiple myelome; application; renal neoplasm; myltiple myelome; application; crohn's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 PREEQYNSTYRVVSVLTVLHQDMLNGKEYKCKVSNKALPSSIEKTISKAK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.1%; Score 558; DB 5; Length 23
95.5%; Pred. No. 1.7e-49;
tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human mutated Fc designated Fc4 protein SEQ ID NO:28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB81491 standard; protein; 232 AA.
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28-JUN-2001; 2001US-0301715P.
29-AUG-2001; 2001US-0315565P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-SEP-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 232 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200238766-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB81491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB81491
                           8866666666666666666666666666666666
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Transmembrane activator; calcium modulator; nephrotropic; antibacterial; TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin; anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive; glomerulonephritis; asthma; bronchitis; graft rejection; septic shock; dermatological; neuroprotective; cyclophilin ligand-interactor; human; autoimmune disease; systemic lupus erythematosus; multiple sclerosis; diabetes mellitus; rheumatoid arthritis; renal disease; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human modified immunoglobulin moiety #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE35220 standard; protein; 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAY-2003
                        Gross JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE35220;
                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                               Local
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The invention relates to fusion proteins comprising transmembrane activator and calcium modulator and cyclophilin ligand-interactor (TACI) receptor group that binds tumour necrosis factor-like protein (ZTNF)2 or ZTNF4; and an immunoglobulin group comprising a constant region of an immunoglobulin. The invention is used to manufacture a medicament for inhibiting the proliferation of tumour cells in a mammalian subject. The composition comprising the fusion protein may also be used in treating autoimmune diseases (e.g. systemic lupus erythematosus, multiple sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft rejection, anaemia and septic shock. The fusion proteins are also used in moiety used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane activator and calcium modulator and cyclophilin ligand-interactor (TACI)-immunoglobulin fusion protein, for treating cancer or diabetes, comprises a TACI receptor group and an immunoglobulin group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Col 110-111; 71pp; English.
                                                                                                                                                                                        24-MAY-2001; 2001US-0293343P.
                                                                                                                                   20-MAY-2002; 2002WO-US015910.
                                                                                                                                                                                                                                             (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                  Gross JA;
                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-148455/14.
                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAD53758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 250 AA;
                          WO200294852-A2.
                                                                               28-NOV-2002.
                                                                                                                                                                                                                                                                                                     Rixon MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ठ
                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a human tumour necrosis factor receptor designated ZunErl2 (1). (1) has cytostatic, immunosuppressive, dermatological, antihifaammatory, neuroprotective, antidabetic, antidatelic, antidatelic, entidatelic, nephrotropic and hypotensive activities, and can be used in gene therapy. (1) can be used for inhibiting, in a mammal, the activity of a ligand that binds ZunErl2 (e.g. ZTNF4), for treating disorders and diseases associated with B completing the proliferation of tumour calls. (1) is useful for treating autoimmune disorders such as systemic lupus erythematosus, myasthenia gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma, theumatoid arthritis, bronchitis, emphysema and end stage renal failure or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid leukaemia, nephritis, and pyelonephritis, and for treating renal coplasms, multiple myelomas, lymphomas, light chain neuropathy, or amyloidosis, hypertension, large vessel disease, graft rejection and Crohn's disease. (1) is useful for modulating the immune system, for regulating a call responses and development, for modulating and cytokine production, and for modulating T and B cell converse communication, Human Zinfirls is located to chromsome 224ja.2 The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence represents a mutated Fc protein designated Fc4, which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 APEAEGAPSVFLFPPRFKDTLMISKTPEVTCVVVDVSHEDPEVRFNWYVDGVEVHNAKTK 75
                                                                                                                                                                                                                     Novel isolated human tumor necrosis factor receptor polypeptide, termed Ztrir 12, useful for treating autoimmune disorders, emphysema, end stage renal failure or renal disease and lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIBKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.1%; Score 558; DB 5; Length 232; 95.5%; Pred. No. 1.7e-49; tive 0; Mismatches 5; Indels
                                                                                       Grant FJ;
                                                                                                                                                                                                                                                                                                                                     Example 4; Page 146; 154pp; English
                                                                                          Xu W, Henne RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 105; Conservative
                                      (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                         WPI; 2002-508212/54.
N-PSDB; ABN89444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 232 AA;
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1 APPVAGGPSVFLFPPKPKDTLMISRTPBVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                94
                                                                      35 APEAEGAPSVFLFPPKPKDTLAISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                            Gaps
                            ô
                                                                                                               61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                 95 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAK
                                                                                                                                                                                                                                                                                                                                 ZTNFR-6; tumour necrosis factor receptor-6; human; 1gG1; Fc cell maturation; bone cell regulation; mutant.
 Length 250;
95.1%; Score 550; DB 6; Length 25
95.5%; Pred. No. 1.8e-49;
live 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Leu in native sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Leu in native sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                    AAY05688 standard; protein; 251 AA
                                                                                                                                                                                                                                                                                                         Modified human IgG Fc sequence.
                                                                                                                                                                                                                                                                               (first entry)
                   Best Local Similarity 95.5
Matches 105, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 41
                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                               19-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                  AAY05688;
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(first entry)

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The present sequence represents a modified human IgG1 Fc region in which the FcgR1 binding site has been mutated from Leu-Leu-Gly-Gly to Ala-Glu-Glu-Ala in order to Feduce FcR1 binding, and residues Ala-134 and Pro-135 have been altered to Ser-134 and Ser-135 to reduce complement Clg binding and/or complement fixation. The mutations were introduced into the native Fc DNA sequence by PCR-mediated mutagenesis (see also AAX5272). The construct was utilised in the preparation of ZTNFR-6-Ig fusion vectors. Solubie ZTNFR-6 (see AAY05679) was expressed in BHK 570 mammalian cells and also in baculovirus sinfected Spodoptera frugiperda Sf9 insect cells. ZTNFR-6 is a novel human tumour necrosis factor receptor. ZTNFR-6 polypeptides are useful for promoting cellular maturation and bone cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 APEABGAPSVFLPPPRPKDTLMISRIPEVTCVVVDVSHEDPBVKFNWYVDGVEVHNAKTX 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZTNPR-5; tumour necrosis factor receptor; TNFR; human; cell maturation; bone cell regulation; IgG1; immunoglobulin; fusion protein; mutant.
                                                                                                                                                                                                                                                                                                                                                   New secreted or membrane bound tumor necrosis factor receptor ZTNFR-6 useful for detecting a genetic abnormality in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 APPVAGGESVFLFPPKPKDTLMISRTPEVTCVVVDVSHBDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PREBOYNSTYRVVSVLTVLHODWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PREEDYNSTYRVVSVLTVIHQDWINGKEYKCKVSNKALPSSIEKTISKAK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 558; DB 2; Length 251;
Pred. No. 1.8e-49;
0; Mismatches 5; Indels
                                'note= "Ala in native sequence"
"Gly in native sequence"
                                                              /note= "Pro in native sequence"
                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Page 138-139; 145pp; English.
                                                                                                                                                                                                                                                                       Gross JA, Matthews SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW97756 standard; protein; 251 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified human IgG1 Fc region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.1%;
ilarity 95.5%;
Conservative 0
                                                                                                                                                           98WO-US018364.
                                                                                                                                                                                        97US-0057608P.
97US-00923725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                       (ZYMO ) ZYMOGENETICS INC.
     /note=
                                                                                                                                                                                                                                                                                                       WPI; 1999-205190/17
                  Misc-difference 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 105; Conserv
                                                                                                                                                                                                                                                                                                                        N-PSDB; AAX25272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 251 AA;
                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAY-1999
                                                                                                                                                           03-SEP-1998;
                                                                                                                                                                                           04-SEP-1997;
                                                                                                                                                                                                          04-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9904001-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
                                                                                            WO9911790-A1
                                                                                                                            11-MAR-1999
                                                                                                                                                                                                                                                                       Farrah TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
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This polypeptide comprises a modified human 1gG1 Fc region. 1gFc cDNA was amplified from a human foetal liver library by PCR (see AAX07230-31). PCR was also used to introduce mutations within the Fc region to reduce FcgRI binding, and to introduce A134G and P135G mutations to reduce complement C1q binding and/or complement fixation (see also AAX07232). Mammalian and abculouirus expression vectors for soluble mutated IgFc were prepared, and used to construct ZTMFR-=—mutated IgFc fusion vectors. ZTMFR-5 (see AAW97749) is a novel human tumour necrosis factor receptor ZTMFR-5. ZTMFR for ligands, agonists and antagonists of ZTMFR-5. The polypeptides can be used in bone cell regulation and to regulate the maturation of TNF ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein; transmembrane activator and CAMI-interactor; tumour necrosis factor; TNF; estif4 activity; antibody production; autoimmune disease; amyloidosis; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis; end stage renal failure; glomerulonephritis; vasculitis; nephritis; renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy; immune response; immunosuppression; graft rejection; joint pain; graft versus host disease; inflammation; swelling; anaemia; septic shock; insulin dependent diabetes mellitus; Crohn's disease; hypertension; renal artery stenosis; occlusion; cholesterol; renal emboli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 APEAEGAPSVFLFPFKPKDTLMISKIPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 APPVAGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPBVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                    Novel tumour necrosis factor receptor ZTNFR5 - useful for regulating maturation of TNF-ligand bearing cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 558; DB 2; Length 25
Pred. No. 1.8e-49;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of the human Fc region.
                                                                                                                                                                                                                                                                                             Example 3; Page 90-92; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB07541 standard; protein; 251 AA
                             98WO-US015072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 95.1%;
Best Local Similarity 95.5%;
Matches 105; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                         (ZYMO ) ZYMOGENETICS
                                                                                                                                                                                    WPI; 1999-132245/11.
                                                                                                                                                                                                      N-PSDB; AAX07232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bearing cells
                                 21-JUL-1998;
                                                                     21-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-OCT-2000
28-JAN-1999
                                                                                                                                              Farrah TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB07541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
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WO200040716-A2

13-JUL-2000.

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07-JAN-2000; 2000WO-US000396.
         07-JAN-1999; 99US-00226533.
                     Xu W, Madden K,
              (ZYMO ) ZYMOGENETICS INC
                           WPI; 2000-452538/39.
                               N-PSDB; AAA58591
                     Gross JA,
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Yee DP;

Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases, renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide. Example 6; Page 170-172; 175pp; English.

A human Pc region polypeptide, which is used in the course of the invention. The specification describes extracellular domains of BR43x2 (an isoform of the transmembrane activator and CAML-interactor (TACI) receptor). TACI or BCAA, (a related B cell protein). These contains a cysteine rich domain, and are used for inhibiting znf4 activity. They may also be used for inhibiting BR43x2. TACI or BCAA receptor—ligand engagement associated with activated or resting B lymphocytes, effector or cells, or with antibody production. The antibody production is associated with an autoimmune disease selected from systemic lupus erythematosus, myasthenia gravis, multiple solerosis and rheumatoid engagement is associated with asthma, bronchitis, erphysema, end stage renal recoplasms, multiple myelomas, light chain neuropathy, amyloidosis, moderating immune response, immunosuppression, graft versus host disease, inflammation, insulin dependent collabetes mellitus, Crohn's disease, inflammation, insulin dependent collabetes malitus, Crohn's disease, inflammation, insuling, anaemia, or septic shock, BR43x2, TACI, and BCAA polypeptides, fusions, antibodies, agonists or antagonists can be used to treat hypertension, renal artery stenosis, or occlusion, and cholesterol or renal emboli

Sequence 251 AA;

0; Gaps tch 35.1%; Score 558; DB 3; Length 251; al Similarity 95.5%; Pred. No. 1.8e-49; 105; Conservative 0; Mismatches 5; Indels Query Match Best Local Si Matches 105;

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PREEQYNSTYRVVSVLTVIAHODWIANGKEYKCKVSNKGLPSSIEKTISKAK 110 61 ຜູ

Search completed: April 29, 2004, 08:44:21 Job time : 51.5 secs

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OM protein - protein search, using sw model

April 29, 2004, 08:41:33 ; Search time 13.5 Seconds (without alignments) 783.783 Million cell updates/sec Run on:

US-09-674-857-3 587 1 APPVAGGPSVFLFPPKPKDT......CKVSNKGLPSSIEKTISKAK 110 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_78:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* 4 01 FC 44

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	ripti	gamma ch	ganma-1	gamma-	heavy ch	gamma-4	датта-2	gamma-3	gamma-3	gamma-	gamma 2b	gamma 2	gamma	heavy ch	gamma 3	gamma	gamma-2b cha	heavy	gamma ch	gamma-2	gamma-1 chain	3 chain	gamma-3	gamma-2 c	gamma-2b	gamma-2b chain	gamma-1 c	gamma-2c chain		monoclonal antibod
		PT0207	531866	СНІНО	869339	G4HU	G2HU	A60764	A23511	G3HUWI	147160	147159	147162	S22080	147161	147158	PS0018	C30554	GHRB	G2GP	831459	G3MSC	G3MSM	806611	G2MSBM	G2MS11	GIMS	S00847	GIMSM	PC4436
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	* Query Match Length DB	234	255	330	374	327	326	377	377	289	328	328	277	470	328	328	333	308	323	329	472	329	398	327	405	474	324	329	393	444
ن	Query Match	94.9	94.9	94.9		94.2	95.6	91.8	91.8	88.4	78.0	78.0	77.2	75.0	73.9	73.9	73.4	71.7	71.7	71.7	71.7	71.2	71.2		•	٠,	67.5		67.5	67.5
	Score	557	557	557	557	553	543.5	m	539	519	458	458	453	440	434	434	431	421	421	421	421	418	418	410	397	σ	σ	396	σ	σ
	Result No.		7	m	4	Ŋ	φ	7	80	σι	10	11	12	13	14	15	16	13	18	19	20	21	22	23	24	25	26	27	28	53

	gamma-za						gamma-2a	gamma-2a	Ig gamma-2b chain		Ig epsilon-chain -	Ig epsilon chain C	Ig gamma-1 chain C	Ig heavy chain pre	Ig epsilon chain C	
GZMSAB	GZMSA	GZMSAM	S37483	801321	840295	PS0017	PS0019	B30503	A30503	146732	136948	EHHO	S14236	S04845	EHRT	
	-		~	N	7	N	N	~	7	N	N	Н	~	7	H	
335	330	399	469	475	446	326	322	112	88	180	426	428	152	549	429	
67.1	9.99	9.99	9.99	65.2	64.9	64.7	57.8	52.6	47.0	42.4	28.5	28.4	27.6	26.7	26.1	
394	391	391	391	383	381	380	339	309		249	167.5	166.5	162	157	153	
30	31	32	33	34	35	36	37	3.8	9	40	41	42	43	44	45	

ALIGNMENTS

RESULT 1

PT0207 g gamma chain C region - chimpanzee C;Species: Pan troglodytes (chimpanzee) C;Species: Pan troglodytes (chimpanzee) C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999 C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999 C;Ancession: PT0207 R;ETT1ch, P.H.; Woustafa, Z.A.; Oestberg, L. Mol: Immunol, 28, 319-322, 1991	A_Tritle: Nuclectide sequence of chimpanzee FC and hinge regions. A,Reference number: PT0207; MUID:91287716; PMID:2062315 A,Accession: PT0207 A,Wolecule type: mRNA A,Residues: 1-234 < EHRP C,Superfamily: immunoglobulin C region; immunoglobulin homology C,Keywords: immunoglobulin F,48-117/Domain: immunoglobulin homology < IMM>	Query Match 94.9%; Score 557; DB 2; Length 234; Best Local Similarity 94.5%; Pred. No. 3.6e-48; Matches 104; Conservative 2; Mismatches 4; Indels 0; Gaps 0; Qy LappvacqpsvrLppprcpcTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60 1	

531866

Iggamma-1 chain C region - synthetic
1g gamma-1 chain C region - synthetic
1,5pecies: synthetic
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Gaps 0 Query Match

94.9%; Score 557; DB 4; Length 255;

Best Local Similarity 94.5%; Pred. No. 4e-48;

Matches 104; Conservative 2; Mismatches 4; Indels

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A, Contents: myeloma protein KOL; disulfide bonds
A, Accession: A91723
A, Molecule type: protein
B, 199-238, 'E', 240,'M', 242-266,'D', 268-271,'D', 273-330 <SC
A, Mote: this sequence has the Gim(3) and Gim(non-1) markers
B, Gall, W.E.; Edelman G.M.
B, Godella tructure of a human gammad-immunoglobulin. X. Intrachain disulfit
A, Reference number: A90565, MUID: 71064027; PMID: 4923144
A, Contents: annotation, disulfide bonds
B, Decker, L.; Schwarz, J.; Reichel, W.; Hlschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A, Title: Rule of antibody structure. The primary structure of monoclonal IgGl immunoglc enbromide cleavage products, and the disulfide bridges.
A, Reference number: A91667, MUID: 77070267; PMID: 1002129
A, Contents: annotation; disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Map position: 14932.33-14932.83
A.Introns: 99/1; 114/1; 224/1
C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into I c.Superfamily: immunoglobulin C region; immunoglobulin homology in menoglobulin peterotetramer; immunoglobulin peterotetramer; immunoglobulin peterotetramer; immunoglobulin homology cIM2-F;20-65/Domain: immunoglobulin homology cIM2-F;23-310/Domain: immunoglobulin homology cIM2-F;23-310/Domain: immunoglobulin homology cIM2-F;23-3144-264,250-308/Disulfide bonds: #status experimental F;103/Disulfide bonds: interchain (to light chain) #status experimental F;103/Disulfide bonds: interchain (to heavy chain) #status experimental
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A,Status: preliminary
A,Molecule type: mRNA
A,Reducs: 1-140, C',142-374 «KH2>
A,Cross-references: EXBL:X81695
C,Superfamily: immunoglobulin C region; immunoglobulin homology
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94.5%; Pred. No. 5.4e-48;
tive 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   557; DB 2;
No. 6.2e-48;
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Pred.
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94.5%;
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Best Local Similarity 94.5'
Matches 104; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: GDB:IGHG1
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A, Contenter: mycloma protein Nie
A, Accession: B9168
A, Accession: B9168
A, Molecule type: protein
A, Residues: 1-34, '0', 35-96, 'K', 98-115, '0', 117-197,' 'D', 199-238,'D', 240,'L', 242-268,'E', 27
A, Residues: 1-34, '0', 35-96, 'K', 98-115, '0', 117-197,' 'D', 199-238,'D', 240,'L', 242-268,'E', 27
A, Note: this sequence has the Glm(17) and Glm(1) markers
R, Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
R, Schmidt, W.E.; Dung, H.D.; Palm, W.; Hilschmann, N.
A, Pritle: Die Primaerstruktur des Kristallisierbaren monoklonalen Immunglobulins IgG1 KOI
A, Reference number: A91723; MUID:83289131; PMID:6884994
                                                                                                APELLGGESVFLFPPKRDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 98
                                                             APPVAGGPSVFLFFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                  m
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A Map position: 1493.33-14932.33

C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into I C; Complex: An immunoglobulin heterotetramer; immunoglobulin C region; immunoglobulin homology C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F; 20.85, Domain: immunoglobulin homology < IMI>
F; 239-206, Domain: immunoglobulin homology < IMI>
F; 239-306, Domain: immunoglobulin homology < IMI>
F; 247-209; 140-200, 246-304, Disulfide bonds: #status experimental
F; 102, 103, 106, 1095/Disulfide bonds: interchain (to heavy chain) #status experimental
F; 102, 103, 106, 1095/Disulfide bonds: interchain (to heavy chain) #status experimental
F; 106, 1095/Disulfide bonds: interchain (to heavy chain) #status experimental
F; 106, 1095/Disulfide bonds: interchain (to heavy chain) #status experimental
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A; Molecule type: protein
A; Residues: 1-24, TE, 26-57, TEV', 60-85;132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198
A; Residues: 1-24, TE, 26-57, TEV', Co. Been revised
R; Hofmann, T.; Parr, D.M.
R; Hofmann, T.; Parr, D.M.
A; Hofmann, T.; Parr, D.M.
A; Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin
A; Reference number: A93132; MUID: 80114419; PMID: 118920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidat
                                                                                                                                                                                                                                                                                                                                                                                                                             A, Molecule type: protein
A, Rolecule type: protein
A, Rolecule type: protein
A, Rolecule Trp-156 is at or near the complement-binding site
A, Note: Trp-156 is at or near the complement-binding site
R, Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A, Title: The amino acid sequences of the three heavy chain constant region domains of
A, Title: The amino acid sequences of the three heavy chain constant region domains of
A, Contents: myeloma protein Zie
A, Contents: myeloma protein Zie
A, A, Rocession: A90752.
                                                                                                                                                                                                                                                                            and
                                  A Molecule type: DNA
A, Molecule type: DNA
A, Molecule type: DNA
A, Redidues: 1-326 GELLA-
A, Cross-references: GB: V00554; GB: J000230; NID: G32759; PIDN: CAB58438.1; PID: g6066056
A, Cross-references: GB: V00554; GB: J000230; NID: g132759; PIDN: CAB58438.1; PID: g6066056
A, Note: Lys-326 is probably removed posttranslationally
R, Manago, A.C.; Tung, B.; Pudebberg, H.H.
G, Immunol. 125, 1048-1054, 1980
A, Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, & A, Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, & A, Contents: myeloma protein Til
A, A, Contents: myeloma protein Til
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Biochem. J. 121, 217-225, 1971
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin A;Feference number: A90255; MUID:72033500; PMID:4944472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Title: Structural studies of immunoglobulin G.
A;Contents: annotation; Sa, disulfide bonds
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Pred. No. 1.2e-46;
5; Mismatches 2;
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A;Cross-references: GDB:119338; OMIM:147110
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A;Mesidues: 238-275 <NOF>
R;HOGmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
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Best Local Similarity 92.7%;
Matches 102; Conservative
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C) Species Home aspless (man)
A; Fills (man)
A; Fills (man)
A; Fills (man)
A; Reference number: A90933; MMID:83157104; PMID:6299662
A; Residues: 1-327 call.
A; Residues: 1-30; Buttery
A; R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 170
                                                                                                                                                             158 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 217
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                                                                            1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
    Gaps
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                                                                                                                                                                                                                                          PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                PREEQYNSTYRVVSVLTVLAQDWLNGKEYKCKVSNKALPADIEKTISKAK 267
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Pred. No. 1.3e-47;
2; Mismatches 4;
Mismatches
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104;
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Best Local S
Matches 104
                                                                                                                                                                                                                                          61
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    Matches
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G2HU
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A;Accession: A9219

A;Accession: A9219

A;Accession: A92219

A;Molecule type: protein

A;Rotesidues: 12-97

A;Note: the hinge region in gamma-3 chains is about four times as long as in other gamm idue segment (12-28)

A;Note: the hinge region in gamma-3 chains is about four times as long as in other gamm idue segment (12-28)

A;Note: the hinge region in gamma-3 chains is about four times as long as in other gamm idue segment (12-28)

A;Note: orgateines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inte

B;Note: orgateines at positions 21, 907-914, 1976

B;Note: partial: The amino acid sequence of "heavy chain disease" protein ZuC. Structure of the

A;Reference number: A90198; MUID: 77021116; PMID: 829945

A;Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues

A;Note: this protein lacks most of the V region, all of the CHI region, and part of the

B;Alexander, A.; Steinnetz, M.; Barritault, D.; Frangione, B.; Franklin, B.C.; Hood, L.

Proc. Mall. Acad. Sci. US.; M. 79, 3260-3264, 1982

A;Title: gamma heavy chain disease in man cDNA sequence supports partial gene deletion

A;Reference number: A99195; MUID: 82247835; PMID: 6808505

A;Contents: Asone as the apports partial gene deletion

A; Accession: Apports partial disease protein Omm

A; Accession: Apports partial gene deletion
                                                                                                                                                                                                                                                                                                                                                                 A.Accession: A50442
A.Molecule type: protein
A.Residues: 1-289 -FRA-
A.Molecule type: protein
A.Residues: 1-289 -FRA-
A.Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain
A.Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain
A.Note: the sequence of residues 42-76 was taken from the reference that follows
R.Michaelsen, T.B.; Frangione, B.; Pranklin, B.C.
A.Biol. Chem. 252, 883-889, 1977
A.Title: Primary structure of the hinge' region of human igg3. Probable quadruplicatic
A.Reference number: A92219, MUID: 7118561; PMID: 402363
A.Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein
                                                C,Date: 31-Dec-1979 #Bequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C,Accession: A90421, A5219, A910188; A93915; A02149
R,Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
Biochemistry 19, 4304-4308, 1980
A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy A;Reference number: A90442; MUID:81021548; PMID:6774747
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPBVKFNWYVDGVEVHNAKTK
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
F;203-270/Domain: immunoglobulin homology rMM-
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental
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es 95; Conserv
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Best Local S:
Matches 95,
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Ig gamma-3 chain C region (allotype G3m(b)) - human
Cippecies: Homo sapiens (man)
Cipace: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C.Accession: A23512
R.Huck, S.; Port, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
R.Huck, S.; Port, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
A.Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: CA; Accession: A23511
A.Molecule type: DNA
A.Accession: A23511
A.Molecule type: DNA
A.Accession: A23511
A.Molecule type: DNA
A.Accession: A3511
A.Molecule type: DNA
A.Accession: A4632.33-14432.33
A.Accession: A4632.33-14432.33
A.Accession: A333-115/3; 130/3; 145/3; 160/3; 270/3
A.Accession: A3511
A.Molecule type: DNA
A.Molecule type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with an IGHG4 convert
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Ig gamma-3 chain C region, form LAT - human
C;Species: Howo sapiens (man)
C;Species: Howo sapiens (man)
C;Species: Howo sapiens (man)
C;Species: Howo sapiens (man)
C;Species: Lefranc, G; Lefranc, G; Lefranc, B;
Z;Huck, S; Lefranc, G; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, bl, c3, c5, u) with an IGHG4
A;Reference number: A60764; MUID: 90007613; PMID: 2571587
A;Accession: A60764
A;Status: preliminary
A;Residues: preliminary
A;Residues: 1-377 cHUC>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Reywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 270
PREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTK 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
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Pred. No. 3.9e-46;
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G3HUWI
IG gamma-3 heavy chain disease proteins - human
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Secure that precursor (B/MT.4A.17.H5.A5) - bovine

NyAlternate names: Ig amma-1 chain Cregion (clone 8.10)
C;Species: Bos primigenius tearus (Cattle)
C;Species: Bos primigenius tearus (Cattle)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S22080; 806610; A31303
R;Sanders, P.G.
Submitted to the EMBL Data Library, November 1991
A;Reference number: $22080
A;Accession: S22080
A;Accession: S22080
A;Accession: S22080
A;Accession: C.A.; Beale, D.
R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
A;Accession: S06610; MUID: 90097956; PMID: 2513487
A;Accession: S06610
A;Molecule Lype: DNA
A;Reference number: $06610; MUID: 90097956; PMID: 2513487
A;Accession: S06610
A;Molecule Lype: DNA
A;Residues: 142-470 csym>
A;Accession: S0610
A;Note: the sequence was determined from the germline gene
C;Genetics:
C;Ge
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147161
R;Kacskovics, I:; Sun, J:; Butler, J.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 GPSAFIFPPRENDITMISRIPROVOVOVOSOBNPSVQESWYDGVEVHTAQTRPKEEQF
                                            A;Residues: 1-277 <KAC>
A;Cross-references: BMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
A;Cross-references: BMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
A;Genetics:
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKPNHYVDGVEVHNAKTKPREEQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                          9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Indels
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                                                                                                                                                                                                                                                                                                                                              ,,
(V)
                                                                                                                                                                                                                                                                                                                                 ch 77.2%; Score 453; DB 2;
1 Similarity 77.9%; Pred. No. 1e-37;
81; Conservative 14; Mismatches
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Matches 79; Conserv
    A, Molecule type: mRNA
A, Residues: 1-277 < KAC>
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local 8
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Matches
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S22080
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19 47159

19 gamma 2a chain constant region - pig (fragment)

C.Species: Bus scrofa domestica (domestic pig)
C.Species: Bus scrofa domestica (domestic pig)
C.Species: 21-eb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C.Accession: 147159

R.Kacskovics, I.; Sun, J.; Butler, J.S.
J. Immunol. 153, 3.565-3573, 1994
A.Title: Five putative subclasses of swine 1gG identified from the cDNA sequences of a A.Reference number: 147158; MUID:95015845; PMID:7930579
A.Rocession: 147159
A.Rocession: 147159
A.Rolecule type: mRNA
A.Rocesidues: 1328 < KAC>
A.Roces-references: EMBL:003779; NID:9433123; PIDN:AAA52217.1; PID:9433124
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C;Accession: 147160
R;KacsKovica, 1.; Sun, J.; Butler, J.E.
A;KacsKovica, 1.3, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Reference number: 147158; MUD:95015845; PMID:7930579
A;Reference number: 147160
A;Accession: 147160
A;Accession: 147160
A;Accession: 147160
A;Coss-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . DB 2; Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: IgG2b
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Gene: igG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <1MM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NSTYRVVSVLTVLHQDWLNGKBYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Score 458; DB
/ Pred. No. 4.1e
14; Mismatches
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Best Local Similarity 78.8%;
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J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine igg identified from the CDNA sequences of a streference number: 147158; MUID:95015845; PMID:7930579
A;Reference number: 147161
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03781; NID:9433127; PIDN:AAA52219.1; PID:9433128
C;Genetics:
A;Gene: CS:
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RESULT 15
147158
19 gamma 1 chain constant region - pig (fragment)
C; Species: Sus scroff domestica (domestic pig)
C; Accession: 147158
R; Kacskovics, 1:; Sun, J; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A; Title: Pive putative subclasses of swine IgG identified from the cDNA sequences of a R, Reference number: 147158
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DBJ
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A; Status: preliminary; tra

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Query Match 73.9%; Score 434; DB 2; Length 328; Best Local Similarity 76.7%; Pred. No. 1e-35; Matches 79; Conservative 13; Mismatches 11; Indels

7 GPSVFLFPPKPXDTLMISRTPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 66 g ò

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Gaps

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67 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKA 109 ò 8

Search completed: April 29, 2004, 08:46:57 Job time : 13.5 secs

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                                                                   April 29, 2004, 08:37:47; Search time 10 Seconds (without alignments) 572.772 Million cell updates/sec
                                                                                                                                           1 APPVAGGPSVFLFPPKPKDT......CKVSNKGLPSSIEKTISKAK 110
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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Maximum Match 100*
Listing first 45 summaries
                                              - protein search, using sw model
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	P04221 oryctolagus P01877 homo sapien					
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ALIGNMENTS

11-UTL-1986 (Rel. 01, Created) 15-WTL-1986 (Rel. 01, Last sequence update) 15-WAR-2004 (Rel. 03, Last annotation update) 16-WAR-2004 (Rel. 03, Last annotation update) 16-WAR-2004 (Rel. 03, Last sequence update) 16HG1. 16HG1. 16HG2. 16HG2. 16HG3. 1
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                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                      WEDLINE=77070267; PubMed=1002129; Dreker L., Schwarz J., Reichel W., Hilschmann N.; Dreker L., Schwarz J., Reichel W., Hilschmann N.; Ended C. antibody structure. The primary structure of a monoclonal Igd1 immunoglobulin (wpeloma protein Nie), I: Purification and Lebrarcterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges."; Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540 (1976).
                                                                                                                                                                                                                            Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970)
                  DISULFIDE BONDS
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21-JUL-1996 (Rel. 01, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
1g gamma-4 chain C region.
1g gamma-4 chain C region.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC...).

R-EMOVED DOST-TRANSLATIONALLY.

K -> R (IN GIM(3) MARKER).

/FIId=VAR 003886.

D -> E (IN GIM(NON-1) MARKER).

FTIG=VAR 003887.

L -> M (IN GIM(NON-1) MARKER).

/FIId=VAR_003889.
            LIGHT CHAIN).
HEAVY CHAIN).
HEAVY CHAIN).
                                                                                                                                                                                                                                                                                                                                               Length 330;
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36106 MW; 3770EB106C2FA33D CRC64;
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1204
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WEDLINE-84235992; PubMed-6329676;
Krawinkel U., Rabbitts T.H.,
"Comparison of the hinge-coding segments in human immunoglobulin gamma
heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Milstein C., Frangione B.; "Disulphide bridges of the heavy chain of human immunoglobulin G2."; Biochem. J. 121:217-225(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=80001357; PubMed=113060;
Connell G.E., Parr D.M., Hofmann T.;
"The amino acid sequences of the three heavy chain constant region
domains of a human IgG2 myeloma protein.";
Can. J. Biochem. 57:758-767[1979].
                                                    Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                  SEQUENCE OF 2-326 FROM N.A.
SEQUENCE OF 2-326 FROM N.A.
MEDLINE=82197621; PubMed=6804948;
Ellison Jw., Rood L.E.;
"Linkage and sequence homology of two human immunoglobulin gamma "Linkage and sequence homology of two human immunoglobulin gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri "Characterization of the two unique human anti-flavin monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 238-275 (ZIE).
MEDLINE=80114419; PubMed=118920;
Hofmann T., Parr D.M.
"A note of the amino acid sequence of residues 381-391 of human
                                                                                                                                                                                                                                                                                                    Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo "Structure of human immunoglobulin gamma genes: implications evolution of a gene family.", Cell 29:671-679(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=81007873; PubMed=6774012; Wang A.-C., Tung E., Fudenberg H.H.; The primary structure of a human 1962 heavy chain: genetic, evolutionary, and functional implications."; Jumunol. 125:1048-1054(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE)
                                                                                                                                                                                                   heavy chain constant region genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REVISIONS TO 25; 59; 60 AND 264-268 (ZIE). Hofmann T., Parr D.M.; Submitted (MAR-1980) to the PIR data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISCLFIDE BONDS.
MEDLINE=69064124; PubMed=5782707;
Frangione B., Milstein C., Fink J.R.L.;
Structural studies of immunoglobulin G.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=7737190;
                                                                                                                                                                                                                                                                          TISSUE=Fetal liver;
MEDLINE=83001943; PubMed=6811139;
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Wol. Immunol. 16:923-925(1979)
                                                Bukaryota, Metazoa, Chordata,
Mammalia, Butheria, Primates,
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                         SEQUENCE OF 88-115 FROM N.A.
Ig gamma-2 chain C region.
IGHG2.
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MEDLINE=95255298; PubMe
                                        Homo sapiens (Human)
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                                                                                                                                                            SEQUENCE OF 1-30 AND 81-326.
MEDLINE-70207560; PubMed=4192699;
Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
"Human immunoglobulin subclasses. Partial amino acid sequence of the Constant region of a gama 4 chain.";
Biochem. J. 117:33-47(1970).
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Pred. No. 1.3e-48;
 Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                      SEQUENCE FROM N.A.
MEDIINE-83157104; PubMed-6299662;
Elison J.W., Buxbaum J.N., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4
DNA 1:11-18(1981).
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35940 MW; 3EDBD811EF208B7A CRC64;
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(Rel. 01, Last sequence update)
(Rel. 40, Last annotation update)
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PIR; A90933; G4HU.
PDB; 1ADQ; 16-SRP-98.
Genew, 147030; 16-SRP-98.
MIM; 147130; 20:0003624; C:membrane fraction; NAS.
GO; GO:0003823; F:antigen binding; TAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003906; Ig-MHC.
Pfam; PF00047; ig; 3.
SWART; SM0407; IG2; 2.
PROSITE; PS50935; IG_IKE; 3.
PROSITE; PS00299; IG_MHC; 2.
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21-JUL-1986;
21-JUL-1986;
16-OCT-2001;
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RESULT 3 GC2 HUMAN ID GC2 H AC P0185 DT 21-JU DT 21-JU

(DISEASE PROTEIN WIS)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 APPVA-GPSVPLFPPKEKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 APPVAGGPSVFLFPPKPRDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                 156 AT OR NEAR THE COMPLEMENT-BINDING SITE.
326 REMOVED POST-TRANSLATIONALLY (PROBABLE)
60 S -> A (IN MYBLOMA PROTEINS TIL & ZIE).

//TICHAR 003889.
109 C -> S (IN REF. 3).
35684 MW; 8310878CG878CF9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini; Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CH3.
INTERCHAIN (WITH A LIGHT CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
11G gamma-3 chain C region (Heavy chain disease protein) (HDC).
                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 326;
                                                                                                                                                                                                                                                                                             CHAIN)
CHAIN)
CHAIN)
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                                                                                                                                                                                                                                                                                            INTERCHAIN (WITH A HEAVY INTERCHAIN (WITH A HEAVY INTERCHAIN (WITH A HEAVY INTERCHAIN (WITH A HEAVY
                                                                                                                                                                                                                     92.6%; Score 543.5; DB 1, 92.7%; Pred. No. 1.2e-47; iive 5; Mismatches 2;
                                                                                 EMBL, J00230; AAB59393.1; --
PIR; A93906; G2HU.
HSSP, POLBS7, 1FC1.
Genew, HWC1:5266; IGHG2.
MIW, 147110;
GO:0005624; C:membrane fraction; NAS.
GO; GO:0003823; F:antigen binding; TAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003906; Ig_AC.
InterPro; IPR003066; Ig_MHC.
Pfam; PF00047; Ig; 3.
SWART; SWO407; IG; 3.
SWART; SWO407; IG; 12.
PROSITE; PS50835; IG_LKE; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 290 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
Nature 221:145-148(1969)
                                                                                                                                                                                                                                         98
3219
326
326
14
102
1103
1106
1109
200
200
304
156
60
                                                                                                                                                                                                                                                                                                                                                                                     109 1
326 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 102; Conserv
                                                                                                                                                                                                                                                   99
220
220
1102
1102
1103
1109
1140
2246
326
60
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P01860;
                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170
                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
GC3 HUMAN
AC PO186
DT 21-UU
DT 21-UU
DT 15-MA
DS IG Ga
GN HGMG3
OC BUXAR
OC MAMMA
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SEQUENCE OF 129-131 AND 155-322
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                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 69.7
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                  NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inmunoglobulin G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
GC RABIT
ID GC RABIT
AC POI870;
                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                 Query Match
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GCB_CB_191 (Rel. 17, Created)
01-FEB_1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
19 gamma-2B chain C region.
If gamma-2B chain C region.
Battus norvegicus (Rat).

Bukaryota; Metazoa Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 APPVAGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                     PYEROLIDONE CARBOXYLIC ACID.
N-LINKED (GLCNAC. . . .)
INTERCHAIN (WITH HEAVY CHAIN DIMER).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FIId=VAR 003896.
E69CBC95705B2P46 CRC64;
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    227
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                                                            MOD_RES
CARBOHYD
DISULETD
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REPEAT
REPEAT
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177
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MEDLINE-76135469; PubMed=1243651;
Praft D.M., Mole L.E.,
"Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype.";
Biochem. J. 151:337-349(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A.
MEDLINE=84030930; PubMed=6313520;
Bernstein K.E., Alexander C.B., Mage R.G.;
Funcleotide sequence of a rabbit IgG heavy chain from the recombinant F.I haplotype.";
Immunogenetics 18:387-397(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10 gamma chain C region.
Oryctolagus cuniculus (Rabbit).
Bukaryota Ketazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Legomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 132-161.
MEDLINE=70110015; PubMed=5461106;
Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
"Sequence studies of the Fd section of the heavy chain of rabbit framed-challin G.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 88-266 FROM N.A.
MEDLINE-8329997; PubMed-6193512;
Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
"Heavy chain genes of rabbit 1gG: isolation of a cDNA encoding heavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                           .,
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(WITH A HEAVY CHAIN).
(WITH A HEAVY CHAIN).
(WITH A HEAVY CHAIN).
                                                                                                                                                                       (WITH A LIGHT CHAIN)
                                                                                                                                                                                                                                                                                                                                                                               73.4%; Score 431; DB 1; Length 333; 69.7%; Pred. No. 2.9e-36; tive 19; Mismatches 14; Indels
36497 MW; 55F8B64D48D460A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        323 AA
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Biochemistry 10:26-31(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Turner K.J., Cebra J.J.;
"Structure of heavy chain from strain 13 guinea pig
immunoglobulin-G42). II. Amino acid sequence of the carboxyl-terminal
and hinge region cyanogen bromide fragments.";
Biochemistry 10:9-17(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 PPVAGGPSVFLFPPXPXDTLMISRTPBVTCVVVDVSHEDPBVKFNWYVDGVBVHNAKTXP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFIDE BONDS.
MEDIATE-71058474;
MEDIATE-71058474;
Diveira B., Lamm M.E.;
"Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
                                                                                                                                                      MEDLINE=71058471; PubMed=5538606;
Birshtein B.K., Hussain Q.Z., Cebra J.J.;
Birshtein B.K., Hussain Q.Z., Cebra J.J.;
"Structure of heavy chain from strain 13 guinea pig
immunoglobulin-G(2). 3. Amino acid sequence of the region around the
half-cystine joining heavy and light chains.";
Biochemistry 10:18-25(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 227-311.
MEDILINE-2036073, PubMed=4609467;
Trischmann T.M., Cebra J.J.;
"Primary structure of the CH3 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tracey D.E., Cebra J.J.; Primary structure of the CH2 homology region from guinea pig IgG2
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERCHAIN (WITH A HEAVY CHAIN)
INTERCHAIN (WITH A HEAVY CHAIN)
INTERCHAIN (WITH A HEAVY CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36074 MW; 5D231B7164D1FBA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.7%; Score 421; DB 1;
71.6%; Pred. No. 2.9e-35;
Live 11; Mismatches 20
                                                                               Trischmann T.M.;
Submitted (APR-1975) to the PIR data bank
                                                                                                                                                                                                                                                                                           SEQUENCE OF 69-133 AND 312-329.
MEDLINE=71058486; PubMed=5538616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 134-226.
MEDLINE=75036072; PubMed=4429665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochemistry 13:4804-4811(1974)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR: A44553; G2GP.
HSSP. POL842; 7FAB.
InterPro; IPR00110; Ig-like.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003506; Ig_MHC.
Pfam; PP00047; ig; 2.
PROM11F; SM0407; IG_L1: 2.
PROSITE; PS06035; IG_LKE: 3.
PROSITE; PS06035; IG_LKE: 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochemistry 13:4796-4803(1974)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 71.6
les 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329 AA;
                  NCBI_TaxID=10141;
                                                                                                                                       SEQUENCE OF 4-68.
                                                          SEQUENCE OF 1-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibodies."
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  8
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                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 PPVAGGPSVFLFPPKPKDTLMISRTPBVTCVVVDVSHBDPBVKFNMYVDGVBVHNAKTKP 61
                                                                           -!- MISCELLANEOUS: Ref.1 sequence has the D12 allotypic marker, 104-Thr, and the B14 marker, 185-Thr. Ref.3 has the D11 and B15 markers and Ref.5 the B15 marker.
-!- SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation contains a canna-2 chain C region.
Cavia porcellus (Guinea pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
(In) Killander J. (eds.);
(Agamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
Stockholm (1967).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 REEQYNSTYRVVSVLTVLHQDWLMGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 REQOPNSTIRVVSTLPITHQDWLRGKEFKCKVHNKALPAPIEKTISKAR 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.7%; Score 421; DB 1; Length 323; 69.7%; Pred. No. 2.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 3.
SMART: SM00407; IGG1; 2.
PROSITE; PSS0835; IG LIKE; 3.
PROSITE; PS00290; IG MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Repeat.
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T -- M (IN DII MARKER).

N -- E (IN REF. 2).

Q -- E (IN REF. 3 AD 4).

N -- D (IN REF. 5).

Q -- E (IN REF. 5).

M -- D (IN REF. 5).

E -- G (IN REF. 5).

E -- G (IN REF. 5).

N -- D (IN REF. 5).

E -- G (IN REF. 5).

Y -- M (IN REF. 5).

N -- D (IN REF. 5).

N -- S (IN REF. 5).
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-> S (IN REF. 5).
69B8AA118D579A8B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IG-LIKE 1.
IG-LIKE 2.
IG-LIKE 3.
                                                                                                                                                                                                                                                                                                                                                                    HSSP, P01857, IRC1.
InterPro, IPR007110, Ig-like.
InterPro, IPR003597, Ig_c1.
InterPro, IPR003006, Ig_MHC.
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PIR: A91749: GHRB.
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323 AA;
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les 75; Conserv
                                                                                                                                                                                                                                                                                                                                                     PIR; A91749;
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P01862;
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CONFLICT
SEQUENCE
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CONFLICT
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VARIANT

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CONFLICT

Query Match

Matches

ద 8 a GC2_CAVPO ID_GC2_C AC_PO186. DT_21-JU DT_15-JU DE_IG_GAVIA OS_CAVIA

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Gaps

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Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                          EMBL; J00451; AAB59655.1; -.
EMBL; V01526; CAA24767.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43929 MW;
                                                                                                                  EMBO J. 3:2041-2046(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
es 76; Conserv
                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCB MOUSE
PO1866,
21-JUL-1986 ()
21-JUL-1986 ()
15-MAR-2004 ()
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GCB_MOUSE
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                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 PP--VAGGPSVFLFPPKPKDTLMISRIPEVTCVVVDVSHEDPBVKFNWYVDGVEVHNAKT 59
                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=85027161; PubMed=6092053; Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Wels J.P., Blattner F.R.; Blattner F.R.; Structural, analysis of the murine 1963 constant region gene.";
      62 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                  RVEQYNTTFRVESVLPIQHQDWLRGKEFKCKVYNKALPAPIEKTISKTK 221
                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P01857; 1FC1.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_Mg.cl.
InterPro; IPR003006; Ig_MHC.
Pfam; PF0047; ig; 3.
PROSITE; PS00836; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Iransmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.2%; Score 41%; DB 1; Length 329; 68.5%; Pred. No. 5.9e-35; ive 15; Mismatches 18; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-0CT-1986 (Rel. 02, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-UUL-1999 (Rel. 18, Last annotation update)
15-gamma-3 chain C region, membrane-bound form.
                                                                                                       01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-COT-2001 (Rel. 40, Last annotation update)
1g gamma-3 chain C region, secreted form.
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CH2.
CH3.
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PIR; B02156; G3MSC.
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Best Local Similarity 60...
Teg 76; Conservative
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113
223
327
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114 2
224 3
329 AA;
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                                                                                                                                                       Mus musculus
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P03987;
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P22436;
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ID GC3M_MC
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                                                                                                                                                                                                                                                                                                                                                     The structure of the mouse immunoglobulin in gamma 3 membrane gene
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MEDLINE=85027161, PubMed=6092053;
MEDLINE=85027161, PubMed=6092053;
Welse J.A., Word C.P., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.M., Blattner F.R.,
"Structural analysis of the murine IgG3 constant region gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A02156; GANSW.
HSSP, P01857; 1FC1.
Interbro; IPR003100; 1g-like.
Interbro; IPR003006; 1g_MHC.
Pfan; P000447; 1g; 3.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00839; IG_MHC, 1.
Imanoglobulin domain; Immunoglobulin C region; Glycoprotein; Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                 SEQUENCE OF 328-398 FROM N.A.
MEDLINE-84041483; PubMed-6314258;
Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.2%; Score 418; DB 1; Length 398; 68.5%; Pred. No. 7.3e-35; Live 15; Mismatches 18; Indels
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B -> G (IN REF. 2).

B -> G (IN REF. 2).

P -> F (IN REF. 2).

CF7F264B50A41B95 CRC64;
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(Rel. 01, Last sequence update)
(Rel. 43, Last annotation update)
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HINGE.
CH2.
CH3.
POTENTIAL.
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RP (AZSOHYDRATE-LINKAGE SITE THR-105.

REDLINE-94216359; PubMed-7512967;

A. M.H. H., Yamaquchi Y., Masuda K., Matsunaga C., Yamamoto K.,

A. M.H. H., Yamaquchi Y., Masuda K., Matsunaga C., Yamamoto K.,

R. A. Timura T., Takahashi W., Redion of mouse immunoglobulin G2b.",

R. "0-glycosylation in hinge region of mouse immunoglobulin G2b.",

J. Biol. Chem. 269:12345-12350(1994).

G. Biol. Chem. 269:12345-12350(1994).

G. SHORTHAITUS PRODUCTS:

C. -I - ALTERNATIVE PRODUCTS:

C. -I - ALTERNATIVE PRODUCTS:

C. Nonce-May be the major isoform;

Name-Secreted;

Isoid=P01865-1; Sequence=External;

C. Nonce-May be the major isoform;

Name-Membrane-bound;

Isoid=P01867-1; Sequence=External;

C. Nonce-May be the major isoform;

Name-Membrane-bound;

Isoid=P01867-1; Sequence=External;

C. -I - PTM: OLINKER GIVANO CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH IS

C. -I - PTM: DISULIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA CHAINS.

C. -I - PTM: DISULIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA CHAINS.

C. -I - PTM: DISULIDE BONDS BY HOMOLOGY WITH OTHER CONSISTS OF GAL-GAL-GALNESOTS;

C. -I - PTM: DISULIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA CHAINS.

C. -I - PTM: DISULIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA CHAINS.

C. -I - PTM: DISULIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA CHAINS.

C. -I - PTM: DISULIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA CHAINS.

C. -I - PTM: DISULIDE BONDS BY HOMOLOGY WITH OTHER Famp.

PIRES SESSOS; GENERAL BROWNS BY HOMOLOGY WITH OTHER BY THE PROPOSITE; PR SEQUENCE FROM N.A. (ALLELE B).
MEDLINE-82173203; PubMed-6803173;
Ollo R., Rougeon F.;
"Mouse immunoglobulin allotypes: post-duplication divergence of gamma 2a and gamma 2b chân genes.";
Nature 296:761-763(1982). SEQUENCE FROM N.A. (MPC 11).
MEDLINE-80081501; PubMed=117548;
Tucker P.W., Marcu K.B., Slightom J.L., Blattner F.R.;
"Structure of the constant and 3' untranslated regions of the murine gamma 2b heavy chain messanger RNA.";
Science 206:1299-1303(1979). SEQUENCE FROM N.A. MEDINE-80081502; PubMed=117549; Pichards J., Blattner P.R.; Tucker P.W., Marcu K.B., Newell N., Richards J., Blattner P.R.; Sequence of the cloned gene for the constant region of murine gamma 2b immunoglobulin heavy chain."; Ig gamma-28 chain u region controllas Mux musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090; SEQUENCE FROM N.A. (ALLELE A).
MEDLINE=80120716; PubMed=6766534;
Yomawaki-Kataoka Y., Kataoka T., Takahashi N., Obata M., Honjo T.;
"Complete nucleoride sequence of immunoglobulin gamma2b chain gene cloned from newborn nouse DNA.";
Nature 283:786-789(1980). IG-LIKE 1. 10-LIKE 2. IG-LIKE 3. INTERCHAIN (WITH A LIGHT CHAIN). CHAIN). (WITH A HEAVY CONTH A HEAVY CO INTERCHAIN INTERCHAIN INTERCHAIN Science 206:1303-1306(1979). DISULFID DISULPID DISULPID DISULPID NON TER DOMAIN DOMAIN NIAMOC

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Gaps

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21; Indels

17; Mismatches

Query Match
Best Local Similarity 65.5
Matches 72, Conservative

Score 397; DB 1; Length 336; Pred. No. 8e-33;

36658 MW; 67.68;

SEQUENCE

(PROBABLE)

O-LINKED (GALNAC. ..).
REMOVED POST-TRANSIATIONALL.
Q - N K IN ALLELE B).
T -> A (IN ALLELE B).
N -> D (IN ALLELE B).
L -> S (IN REF. 2 AND 3).
L -> S (IN REF. 2 AND 3).
S -> P (IN REF. 2 AND 3).
I -> T (IN REF. 2 AND 3).
I -> T (IN REF. 2 AND 3).
Hy 7D879662607C356E CRC64;

1118 210 3114 1105 336 300 301 25 239

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INTERCHAIN (WITH A HEAVY CHAIN)

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SEQUENCE OF 70-322 FROM N.A. (MYBLOMA PROTEIN MOPC 21).
MEDINE=80012837; Pubmed=113776;
RSOgers J., Clarke P., Salser W.;
*Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                                                                                                                                                                                                            DISULPIDE BONDS (MOPC 21).
MEDLINE=73008889; PubMed=5073237;
MISTERIO C., Milstein C.;
The disulphide bridges of a mouse immunoglobulin Gl protein.";
Blochem. J. 126:837-850(1972).
-!- SUBCELLULAR LOCATION: Secreted.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                         Adetugbo K.;
"Evolution of immunoglobulin subclasses. Primary structure of
"Evolution of gammal chain.";
J. Biol. Chem. 253:6068-6075(1978).
                                                                                                                                                                                                                                                                                                                                                                                         Name=Secreted;
Isold=Pol866-1; Sequence=Displayed;
Note=May be the major isoform;
Name=Membrane-bound;
                                                                                      Yucleic Acids Res. 6:3305-3321(1979).
                                                                                                                      SEQUENCE (MYELOMA PROTEIN MOPC 21).
MEDLINE=78242288; PubMed=98524;
                                                                         heavy chain.
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MEDILINE-80202559; PubMed=6769752;
Obbita M., Vamawaki.Kataoka Y., Takahashi N., Kataoka T., Shimizu A., Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";
Gene 9:87-97(1980).
                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15 gamma-1 chain C region secreted form.
Mus musculus (Mouse).
Bukaryota; Mctazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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MEDLINE-BROODSOS; PubMed=115593;

Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
Takahashi N., Mano Y.;
Groning and complete nucleotide sequence of mouse immunoglobulin
Gamma I Chain gene.";
Cell 18:559-568 (1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.6%; Score 397; DB 1; Length 405; 65.5%; Pred. No. 9.9e-33; ive 17; Mismatches 21; Indels
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405 CYTOPLASMIC (POTENTIAL).
44330 MW; 89B3CF0A9B6D49FA CRC64;
   send an email to license@isb-sib.ch).
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P01868;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PP00047; ig; 2.
SMART; SM00407; IGcl; 2.
PROSITE; PS50825; IG_LIKE; 3.
PROSITE; PS02290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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N -> D (IN REF. 3).
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276 N -> D (IN REF. 3).
278 N -> D (IN REF. 3).
35704 MW; A338812F3D1F2C93 CRC64;
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IsoId=P01869-1; Sequence=External;
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HINGE.
CH2.
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EMBL, V00793, CAA24173.1; ---
EMBL, V00793, CAA24173.1; ---
EMBL, V00793, CAA24175.1; ---
EMBL, V00795, CAA24175.1; ---
EMBL, V00795, CAA24175.1; ---
EMBL, V00795, CAA24175.1; ---
EMBL, V00795, CAA24176.1; ---
INF, A02159, G1MS.

ADD, MGT.96466, IGh-4.
InterPro; IPR007110; IG-like.
InterPro; IPR0073597; IG-like.
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67.6%; Pred. No. 9.7e-33; ive 19; Mismatches 14; Indels

Best Local Similarity 67.69 Matches 69; Conservative

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MEDIATR=8222190; PubMed=6283537;
MEDIATR=82222190; PubMed=6283537;
"Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982). 21-JUL-1986 (Rel. 01, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g gamma-1 chain C region, membrane-bound form.
Mus musculus (Mouse).
Exaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
11 TaxID=10090; SEÇUENCE FROM N.A.
MEDLINE=80045036; PubMed=115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
"Cloning and complet nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
Cell 18:559-568(1979). SEQUENCE OF 323-393 FROM N.A. MEDIJNE=82197626; PLDMed=6804950; Tyler B.M., Cowann A.P., Gerondakis S.D., Adams J.M., Bernard O.; Tyler B.M. for surface immuncalobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular SEQUENCE OF 323-366 FROM N.A.
MEDLINE=82115295; PubMed=6799207;
Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl
Eisenberg D., Wall R.;
Gene segments encoding transmembrane carboxyl termini of
immunoglobulin gamma chains."; Event=Alternative splicing; Named isoforms=2; domain."; Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982) Name=Membrane-bound; IsoId=P01869-1; Sequence=Displayed; Isold=P01868-1; Sequence=External; Note=May be the major isoform; EMBL, V00793; CAA24172.1; -. EMBL, V00793; CAA24173.1; -. EMBL, V00793; CAA24174.1; -. PIR; B02159; GIMSM. STANDARD; 15C8; 23-MAR-99. 1AB6; 18-MAR-98. 1CL7; 12-JAN-00. 06-FEB-01. 29-DEC-99. 24-JUL-02. Name=Secreted; GCIM MOUSE P01869; EMBL; EMBL; PIR; B PDB; 1 PDB; PDB; PDB; This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch) 65 6 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBI_TaxID=10116; Brueggemann M., Delmastro-Galfre, P., Waldmann H., Calabi F., "Sequence of a rat immunoglobulin gamma 2c heavy chain constant region cDNA: extensive homology to mouse gamma 3."; Eur. J. Immunol. 18:317-319(1988). ö CH3. INTERCHAIN (WITH A LIGHT CHAIN) INTERCHAIN (WITH A HEAVY CHAIN)
INTERCHAIN (WITH A HEAVY CHAIN) Length 329; YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110 67.5%; Score 396; DB 1; Length 32 67.6%; Pred. No. 9.9e-33; ive 17; Mismatches 17; Indels 69 TYRVVSVLTVLHQDWLNGKBYKCKVSNKGLPSSIEKTISKAK 110 176 TFRSVSELPIMHODMLNGKBFKCRVNSAAFPAPIEKTISKTK 217 36571 MW; 5FCD7B7933850773 CRC64; HSSP, D01842; TRAB.
INTERPRO; IRR007110; Ig-like.
INTERPRO; IRR007106; Ig_c1.
INTERPRO; IRR003006; Ig_MC.
PERM; PR0047; ig_. 2.
SWART; SW00407; Igc1, 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MC; 1. 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-2C chain C region.
Rattus norvegicus (Rat). 329 AA CH1. HINGE. CH2. SEQUENCE FROM N.A. MEDLINE=88166903; PubMed=3127222; EMBL; X07189; CAA30169.1; -. PIR; S00847; S00847. Conservative STANDARD; 111 113 143 249 329 AA; Local Similarity ses 71; Conserv

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SEQUENCE Query Match

Best Loca Matches

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Search completed: April 29, 2004, 08:44:53 Job time : 10 secs
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**A MEDLINE=82037777; PubMed=6794027;

**A Dognin M.J., Lauwereys M., Strosberg A.D.;

**RT MULLIPle amino acid substitutions between murine gamma 2a heavy chain Fo regions of Igla and Igla allotypic forms.";

**RT F.D.** Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).

**CC -!- SUBCELLULIAR LOCATION: Secreted (Potential).

**CC -!- ALTERNATIVE PRODUCTS:

CC -!- ALTERNATIVE PRODUCTS:

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21-UU-1986 (Rel. 01, Last sequence update)
15-MAR-2004 (Rel. 01, Last sequence update)
15-MAR-2004 (Rel. 43, Last amoutation update)
19 Gamma-2A chain C region secreted form (B allele).
Mus musculus (Mouse).
Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
VCBI_TaxID=10090;
R PDB; IXCR; 11-MAY-02.
R PDB; 25C6; 09-JUL-99.
R MGD, MGI:96446; Igh-4.
R InterPro; IPR00110; Ig-like.
R InterPro; IPR0013597; Ig_C1.
R InterPro; IPR003597; Ig_C1.
R PFBM; PF00047; ig; 2.
R PKART; SW00407; IgC1: 2.
R PKOSITE; PS002596; IG_LIXE; 3.
R PROSITE; PS00299; IG_MRC; 1.
N Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; M Alternative splicing; Transmembrane; 3D-structure.
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INTERCHAIN (WITH A HEAVY CHAIN).
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MEDLINE=82037861; PubMed=6170065;
MEDLINE=82037861; PubMed=6170065;
"Miltiple differences between the nucleic acid sequences of IgG2aa and IgG2ab alleles of the mouse.";
Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               $; Score.396; DB 1; Length 393;
b; Pred. No. 1.2e-32;
19; Mismatches 14; Indels
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CYTOPLASMIC (POTENTIAL).
4CC88343B7A1CE27 CRC64;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                           IsoId=P01865-1; Sequence=External;
-!-MISCELANBOOS: The sequence differs from that of the a allele,
from BALB/c mice, at 15% of the positions.
-!- SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PREEDYNSTYRVVSVLTVLHQDWLNCKEYKCKVSNKGLPSSIEKTISKAK 110
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Best Local Similarity 64.5%; Pred. No. 1.6e-32;
Matches 71; Conservative 18; Mismatches 21; Indels
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126 225 16-LIKE 2.
234 330 IG-LIKE 3.
335 AA, 36596 MM, PA3382792CBB13C6 CRC64;
IsoId=P01864-1; Sequence=Displayed;
Note=Probably the major isoform;
Name=Membrane-bound;
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1 APPVAGGPSVFLFPPKPDT......CKVSNKGLPSSIEKTISKAK 110
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q7z7p5 homo sapien	Q7z5w1 homo sapien	Q7z351 homo sapien	Q96pq8 homo sapien	Q8tc63 homo sapien	Q86tt2 homo sapien	Q8nf17 homo sapien	Q8n4y9 homo sapien	Q95m34 equus cabal	Q7tmkl mus musculu	Q8r3v9 mus musculu	Q91z05 mus musculu	Q8r3h6 mus musculu	Q9rla4 mus musculu	Q991c4 mus musculu	Q9d814 mus musculu
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ALIGNMENTS

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PRELIMINARY;
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(TrEMBLrel. 25, al protein. 482 AA; 5 Homo sapiens (Human) SEQUENCE FROM N.A. NCBI_TaxID=9606; Q7Z351 PP Q7Z351; 01-OCT-2003 (SECUENCE RESULT 3 Q7Z351 253 APELLGGPSVFLFPPREXDYCHMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTK 312 9 Gaps Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606; ö Length 469; Indels 01-0CT-2003 (TrEMBLrel. 25, Created) 01-0CT-2003 (TrEMBLrel. 25, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update) Hypothetical protein. Homo sapiens (Human)

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RESULT 4

Homo sapiens (Human). Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TREMBLrel. 25, Last annotation update)
Pactor VII active site mutant immunoconjugate. PRELIMINARY; 80496D

"Targeting tissue factor on tumor vascular endothelial cells ar cells for immunotherapy in mouse models of prostatic cancer."; Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001). MEDLINE=21477448; PubMed=11593034; Hu Z., Garen A.; SEQUENCE FROM N.A. NCBI_TaxID=9606;

and tumor

Hu Z., Garen A.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AF272774, AAKS6666.2;
CO, GO:0005576, C:extracellular, IEA.
GO, GO:0004263; F:calcium ion binding; IEA.
GO, GO:0004263; F:chymotrypsin activity; IEA.
GO, GO:0004263; F:trypsin activity; IEA.
GO, GO:0004269; F:trypsin activity; IEA.
GO, GO:0004295; F:trypsin activity; IEA.
InterPro; IPR000152; Asx hydroxyl S.
InterPro; IPR004042; GSF 2.
InterPro; IPR001691; GSF 2.
InterPro; IPR001891; GSF 2. SEQUENCE FROM N.A.

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1 APPVAGGPSVFLFPPKPKDTIMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK Gaps TISSUE-Human rectum tumor;
Bloecker H., Boecher M., Mewes H.N., Weil B., Amid C., Osanger A., Flob G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX538118; CADS9026.1; -.
Hypothetical protein. 326 PREEQYNSTYRVVSVLTVLAQDWLNGKEYKCKVSNKALPAPIEKTISKAK 375 ő Length 482; Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo Score 557; DB 4; Lengtn au. Pred, No. 9.3e-54; "''marches 4; Indels 52852 MW; EDA75F1901D1A034 CRC64; 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein DKFZp686N02209.
DKFZp686N02209. Query Match
94.9%; Score 557; DB
Best Local Similarity 94.5%; Pred. No. 9.3e
Matches 104; Conservative 2; Mismatches Created)

Strausberg R.; Strausberg R.; Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases. BMBL; BC051328; AAH51328.1; -. Hypothetical protein. SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAP795C CRC64;

Query Match SYNER

Query Match 94.9%; Score 557, DB 4; L Best Local Similarity 94.5%; Pred. No. 9e-54; Matches 104; Conservative 2; Mismatches 4;

셤 ठे Db

1 APPVAGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK

PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110 61

PRELIMINARY; 07Z5W1

SEQUENCE FROM N.A. RESCULT 2
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TISSUE=Spleen

NEDLINE=22388257; PubMed=12477912;

NEDLINE=22388257; PubMed=12477912;

Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

A lausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A litschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A patchench L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carminci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McZwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A lalton D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Jones S.J., Marra M.A.,

T "Generation and initial analysis of more than 15,000 full-length human

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002) and mouse cDNA sequences.

Strausberg R.; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases. SEQUENCE FROM N.A. rissum=Spleen;

EMBL, BCD53984; AAH53984.1; -. Hypothetical protein. SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

DB 4; Length 470; 4; Indels 94.9%; Score 557; DB 4; 94.5%; Pred. No. 9e-54; ive 2; Mismatches Best Local Similarity 94.5 Matches 104; Conservative Query Match

1 APPVAGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK

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61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110

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Thu Apr 29 09:15:48 2004
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18-09-6/4-85/-3.TSDT

Gaps

4; Indels

Length 473;

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257 APEFLGGSAVPLPPPKDKDTLMISRTPEVTCVVVDVSQEDFEVQENWYVDGVEVHNAKTK 316
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 APPVAGGPSVFLFPPKDKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWART; SM00406; IGV; 1.
PROSITE; PS00196; COPPER BLUE; 1.
PROSITE; PS00290; IG_LIKE; 4.
BYDOSITE; PS00290; IG_MHC; 3.
Hypotherical protein.
SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;
                                                                                                                                                                                                                                                                             Ouery Match

94.2%; Score 553; DB 4;
Best Local Similarity 94.5%; Pred. No. 2.6e-53;
Matches 104; Conservative 2; Mismatches 4
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SEQUENCE FROM N.A.
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TISSUE=Placenta;
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Q86TT2
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QBNF17
ID QBNF
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R InterPro; IPR001438; BGF_II.
R InterPro; IPR00209; EGF_like.
R InterPro; IPR002109; EGF_like.
R InterPro; IPR002101; IgadF_lood.
R InterPro; IPR001201; IgadF_like.
R InterPro; IPR001201; IgadF.
R InterPro; IPR001201; IgadF.
R InterPro; IPR001201; Peptidase_S1A.
R InterPro; IPR001204; Peptidase_S1A.
R InterPro; IPR001204; VitK_dep_GLA.
R Pfam; PF00009; EGF; 2.
R Pfam; PF00009; EGF; 2.
R Pfam; PF00009; EGF; 2.
R PRINTS; PR00010; EGFBLOOD.
R RNART; SN00101; GLABLOOD.
R SNART; SN00101; GLABLOOD.
R SNART; SN00100; EGFBLOOD.
R SNART; SN00100; EGFBLOOD.
R SNART; SN00100; EGFC_A; 1.
R PRINTS; PR00101; AZK_HYDROXYL; 1.
R PROSITE; PS00101; AZK_HYDROXYL; 1.
R PROSITE; PS01017; EGF_CA; 1.
R PROSITE; PS01017; TRYPSIN_IN; 1.
R PROSITE; PS010187; EGF_CA; 1.
R PROSITE; PS010187; TRYPSIN_INSR; 1.
R PROSITE; PS010187; TRYPSIN_ER; 1.
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086TT2;
01-UN-2003 (TrEMBLrel. 24, Created)
01-UN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Human Lull-length cDNA clone CS0D1019YF20 of placenta of Homo sapiens
(Human) (Fragment).
Homo sapiens (Human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Living B. Gruber C., Jessee J., Polayes D.;

In W. B., Gruber C., Jessee J., Polayes D.;

"Full-length cDNA libraries and normalization.";

"Full-length cDNA libraries and normalization.";

"Full-length cDNA libraries and normalization.";

"Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

REMBL; BX248278; CAD62606.1; -.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR003006; Ig_MHC.

R PROSITE; PS00290; IG-LIKE; 3.

R PROSITE; PS00290; IG_MEC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 91.8%; Score 539; DB 4; Length 35
Best Local Similarity 90.9%; Pred. No. 6.6e-52;
Matches 100; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                  Genoscope, Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER 1 1
SEQUENCE 354 AA; 39125 MW; 23B80BF4D2B87A92 CRC64;
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354 AA
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PRELIMINARY;
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095M34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 APPVAGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical profesin.
Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Spleen,
Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
"The nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                                                                                                                         Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
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C TISSUE=Primary B-Cells;
Strausberg R.;
L Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
R EMBL; BC033178; A4H33178.1; -..
R INTERPO: JPR001710; Ig-like.
R SMART; SM0040; Ig-MHC.
R SMART; SM0040; IG-Like; Ig-v.
R PROSITE; PS50835; IG LIKE; 4.
R PROSITE; PS50835; IG LIKE; 4.
R HYPOCHACICAL DOCCOL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 535; DB 4; Length 50
Pred. No. 2.9e-51;
5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       509 AA; 56111 MW; 089498D8076E863C CRC64;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
FLJ00385 protein (Fragment).
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Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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Best Local Similarity 90.05
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                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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SEQUENCE
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Q8N4Y9;
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MEDLINE-99383416; PubMed-9717671;

MEDLINE-99383416; PubMed-9717671;

MEDLINE-99383416; PubMed-9717671;

MEDLINE-99383416; PubMed-9717671;

MEDLINE-99383416; PubMed-9717671;

MEDLINE-9016 W., Radbruch A.;

"Organization of the equine immunoglobulin heavy chain constant region genes. II. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";

In munobiology 199:105-119(1998).

EMBL; AJ300675; CAC44624.1; -...

RICEPRO; IPR003209; IG_LIKe.

InterPro; IPR003209; IG_LIKe.

RICEPRO; IPR003209; IG_LIKE.

REMEN: PR0047; IGC1; 2.

REMEN: PR0047; IGC1; 2.

REMEN: PR0047; IGC1; 2.

REMEN: PR0051TE; PS00230; IG_MHC; 2.
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                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Buks musculus (Mouse).
Bukaryots, Metazca; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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Bukaryota; Metazoa (hordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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                                                                                                                                                                                                                                                     61 PREEDYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEG-2001 (TrEMBLrel. 19, Created)
01-DEG-2001 (TrEMBLrel. 19, Last sequence update)
01-DGT-2003 (TrEMBLrel. 25, Last annotation update)
Immunogobulin gamma 1 heavy chain constant region (Fragment)
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Query Match 91.1%; Score 535; DB 4; Length 521;
Best Local Similarity 90.0%; Pred. No. 3e-51;
Matches 99; Conservative 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wagner B.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               337 AA
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RESULT 12
Q91205
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                                                 SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.

SEQUENTE-2188257, PubMed=1247932;

KITAIN=CZECH II, TISSUE=Breast tumor;

KITAIN=CZECH II, TISSUE=Breast tumor;

KITAIN=CZECH II, Felingold E.A., Grouse L.H., Derge J.G.,

KITAIN=CZECH II, TISSUE-Breast L. Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeberg B., Buetow K.H., Schaefer C.F., Bhala N.K.,

Hopkins R.F., Jordan H., Moore T., Max J., Wang J., Heiseh F.,

Astaplaton M., Soares M.B., Bonaldo M.F., Casvaninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,

Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakeley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     253 PPGNILGGPSVFIFPPKDALMISLIPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWT 312
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313 QPREAQYNSTFRVVSALPIQHQD#MRGKEFKCKVNNKALPAPIERTISKPK 363
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71.2%; Score 418; DB 11; Length 470;
Best Local Similarity 68.5%; Pred. No. 3.4e-38;
Matches 76; Conservative 15; Mismatches 18; Indels
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Submitted [MAR-2002) to the EMBL/GenBank/DDBJ databases.
Submitted [MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL. BC02440; AAH24405.1; -.
PIR; B45837; B45837.
WGD; MGI:96446; Igh-4.
InterPro; IPR001010; Ig-like.
InterPro; IPR003006; Ig-w.
Pfan; PR00047; Igi. 3.
SWART; SW00406; IGv. 1.
PROSITE; PS50835; IG_LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
BMBL, BC055910; AAH55910.1; -.
Hypothetical protein.
SEQUENCE 470 AA; 51727 MW, 6D90E4DF896BB090 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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SEQUENCE FROM N.A.
STRAIN-CZECH II; TISSUE-Breast tumor;
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01-JUN-2002 (TrEMBLES 21,
01-OCT-2003 (TrEMBLES 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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WCBI_TaxID=10090;
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008R3V9
AC Q8R3V
AC Q8R3V
DT 01-JU
DT 01-JU
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DE HYPOT
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DE NAME TO
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                                                                                                                     Gaps
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
VCBI_TaxID=10090;
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                                                                             Length 469;
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Submitted (JUL-2011) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2011) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010327; AAH10327.1; -
NGD; MGI:2144967; AA0044919.
CGO: GO:0005489; F:electron transporter activity; IEA.
CGO: GO:0006118; P:electron transport; IEA.
InterPro; IPR007110; IG-11xe.
InterPro; IPR007110; IG-11xe.
InterPro; IPR003596; IG-V.
Pfam; PP00047; IG:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.6%; Score 397; DB 11; Length 4
65.5%; Pred. No. 7.6e-36;
live 17; Mismatches 21; Indels
                                                                                                                                                                                                                                               69 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                   321 TFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTK 362
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     il protein.
473 AA; 51946 MW; CF625F008932AF12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
                                                                           Query Match
Best Local Similarity 68.6%; Pred. No. 3.5e-36;
Matches 70; Conservative 18; Mismatches 14;
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PROSITE; PSO0190; CYTOCHROME (
PROSITE; PS50835; IĞ LIKE; 4.
PROSITE; PS00290; IĞ_MHC; 1.
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nes 72; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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01-70N-2002 (TrEMBLrel.
01-70N-2002 (TrEMBLrel.
01-0CT-2003 (TrEMBLrel.
Hypothetical protein.
AU044919. (Mouse).
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AU044919.
Mus musculus (Mouse).
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AN 141
REPORTING FROM N.A.
Rilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
Rilde Gonstruction of a stringle chain antibody (ScFV).";
Rilde K.M.Y.1993) to the EMBL/GenBank/DDBJ databases.
BRHIL, AF152372; AAD40243.1; -.
BRHIL, PROSTIC PRO03006; IQ-Hike.
BRHIL, PRO03006; IQ-Hike.
BRHIL, PRO03006; IG-Hike.
BRHIL, PRO0317E; PS00230; IG-HIKE; 4.
BRHILL PROSTIE; PS00230; IG-HIKE; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 APNLEGGESVFIFPPNIKDVLMISLTPRVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQ 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 APPVAGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musimae, Mus.
VCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PREEDYNSTYRVVSVLTVLHQDWLMGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             318 THREDYNSTIRVVSALPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIK 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.6%; Score 397; DB 11; Length 474; 65.5%; Pred. No. 7.6e-36; tive 17; Mismatches 21; Indels
                                                                                                                                                         A Strausberg R.;

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

R EMBL; SCOS2447; AAH25447.1;

R MGD; MGI:2144697; AUGH4919.

R GO; GO:0006518; F:electron transporter activity; IEA.

R GO; GO:0006118; P:electron transport; IEA.

R InterPro; IPR000345; Cy-C, heme_BS.

R InterPro; IPR000345; Cy-C, heme_BS.

R InterPro; IPR000359; Ig-V.

R InterPro; IPR003596; Ig-V.

R InterPro; IPR003596; Ig-V.

DR PMART; SN00406; IGV; 1.

DR PROSITE; PS00190; CYPOCHROME_C; 1.

PROSITE; PS00190; CYPOCHROME_C; 1.

PROSITE; PS00390; IG_MHC; 1.

KW Hypothetical protein.

SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5C3A7BB3EE7D697C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAY-2000 (TrEMBLrel. 13, Created)
1-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-GCT-2003 (TrEMBLrel. 25, Last annotation update)
Gammal heavy chain of Mab7 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 65.5%; Pred. No. 7.6e
Matches 72; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48142 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          437 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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SEQUENCE
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Q9R1A4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.5%; Score 396; DB 11; Length 463; 67.6%; Pred. No. 9.6e-36; tive 19; Mismatches 14; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                   Straubberg R.;
Straubberg R.;
Straubberg R.;
Straubberg R.;
Straubberg R.;
Straubberg R.;
EMBL; BC001345; AAH03435.1;
PIR, B45837; AAH03435.1;
RISSP; P01842; TFAB.
MGD; MGI: 96446; IGH-4.
InterPro; IPR001010; Ig-1ike.
InterPro; IPR001006; Ig-MHC.
InterPro; IPR001006; Ig-W.
Pfam; P070047; Ig-3.
SWART; SM04406; IGV; 1.
PROSITE; PS050835; IG-LIKE; 4.
PROSITE; PS050835; IG-LIKE; 4.
PROSITE; PS050836; IG-LIKE; 4.
SEQUENCE 463 AA; 51007 MW; EAA674C6BEC30783 CRC64;
                                                                                      289 TFRSVSELPIMHODWLNGKEPKCRVNSAAFPAPIEKTISKTK 330
                                                               69 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 TYRVVSVLTVLHQDWLNGKBYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                              Similar to RIKEN cDNA 1810060009 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 67.68
Matches 69; Conservative
                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                  IGH-4.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                          Q99LC4;
                                                                                                                                                                                       099LC4
                                                                                                                                                       RESULT 15
                                                                                                                                                                          Q99LC4
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Search completed: April 29, 2004, 08:46:18 Job time : 37 secs

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Gabs

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14; Indels

67.5%; Score 396; DB 11; 67.6%; Pred. No. 8.9e-36; tive 19; Mismatches 14;

Query Match Best Local Similarity 67.6% Traches 69; Conservative

Length 437;

89

9 SVFLFFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

April 29, 2004, 08:46:23 ; Search time 38.5 Seconds (without alignments) 791.970 Million cell updates/sec Run on:

US-09-674-857-3 587

1 APPVAGGPSVFLFPPKPKDT......CKVSNKGLPSSIEKTISKAK 110 Perfect score:

BLOSUM62 Scoring table: Sequence:

1138120 segs, 277189581 residues Searched:

Gapop 10.0 , Gapext

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2 6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2 6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
3: /cgn2 6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2 6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2 6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2 6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
7: /cgn2 6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
8: /cgn2 6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2 6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2 6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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17: /cgn2 6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2 6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Appl	Appl	Appl	Appl	Appl	Appli	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl
	22,	22,	67,	12,	10,	~ ~	90,	28,	32,	35,	31,	33,	42,	62,	52,
Description	Sequence	Seguence	Seguence	Seguence	Sequence	Seguence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence
ID	US-09-932-812-22	US-09-968-362-22	US-10-071-485-67	US-10-683-255-12	US-10-683-255-10	US-10-683-255-8	US-10-071-485-90	US-10-008-063-28	US-10-008-063-32	US-10-152-363A-35	US-10-152-363A-31	US-10-152-363A-33	US-10-008-063-42	US-10-152-363A-62	US-10-152-363A-52
DB	101	10	14	12	Z	۲ ا	현	14	14	74	14	14	14	14	14
% Query Match Length	435	447	468	488	497	525	711	232	232	250	251	251	328	332	344
% Query Match	97.1	97.1	95.7	95.7	95.7	95.7	95.7	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1
Score	570	570	562	562	562	562	562	558	558	558	558	558	558	558	558
Result No.	<u></u>	7	m	4	5	9	7	æ	σv	10	11	12	13	14	15

RESULT 2 US-09-968-362-22 ; Sequence 22, Application US/09968362

ppl	[ddi	ppl	pp]	Appl	ĭpp1	lpp1	ippi	tpp1	lpp1	ippl	lpp1	(pp)	ld(\ppl	\ppl	'pl	\ppl	lggv	/pp]	upp]	(dd)	(pp)	ilg	Αp	ipli	pli	pli	p_{1i}	Appli
54	26,	20,	, 20,	20,	23,	S	23	62	63	Ö	61	62	62,	99	e 62	23,	24	23	69	9,0	9	23	ď	42	ei O	e 2,	ų	ς,	ŗ,
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Seguence	Seguence	Seguence	Sequenc	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguenc	Sequence	Sequenc
-10	-10	10	-09	US-09-968-362-20	US-09-995-898A-23	-10	-09	US-10-104-919-62	-10	-09	-10	US-10-395-741B-62	US-09-746-359A-62	US-09-951-268-39	US-10-424-658-62	4	9-951	10-424-658-2	-09-892-949-6	10-352-554-3	-10-351-157-	10-370-749-2	10-033-	-10-264-	-60-	-09-813-341-	10-277-	-10-277-307	US-10-277-370-1
4						12			16	10	14	G		12	15		N	15			15	15	13	15	12	7	14	14	14
348	357	392	437	449	473	473	476	476	476	484	484	484	559	559	559	594	594	594	764	764	764	110	212	215	218	218	218	218	218
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558	558	558	558	558	558	558	558	558	558	558	558	558	558	558	558	558	558	558	558	558	558	557	557	557	557	557	557	557	557
16	17	18	13	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	4,	42	43	44	45

ALIGNMENTS

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Sequence 22, Application US/09932812
Publication No. US20030082749A1
Publication No. US20030082749A1
GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Cecily R
APPLICANT Sun, Cecily R
APPLICANT Sun, Cecily R
APPLICANT Sun, Cecily R
APPLICANT Sun, Cecily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: HUBPO-L-vFc gammal with a 27-amino acid leader peptide (Figure 2 US-09-932-812-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 APPVAGGPSVFLPPPKPKDTLMISRTPBVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 97.1%; Score 570; DB 10; Length 435; Best Local Similarity 97.3%; Pred. No. 1.6e-50; Matches 107; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence FEATURE:
RESULT 1
US-09-932-812-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT
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272 APELEGGESVFLFPPKPKDTIMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK 331
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61 PREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   332 PREEQYNSTYRVVGV5TVLHQDMLNGKEYKCKVSNKALPASIEKTISKAK 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 488;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
US-10-683-255-10
Sequence 10, Application US/10683255
Publication No. US20040063910A1
GENBEAL INFORMATION:
APPLICANT: Ravanaugh, William M.
APPLICANT: Ballinger, Marcus
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
FILE REFRENCE: PPO.4474.101
CURRENT APPLICATION NUMBER: US/10/683,255
CURRENT FILING DATE: 2003-10-10
FRIOR FILING DATE: 2003-10-10
FRIOR FILING DATE: 1999-02-08
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 497
                                                                                                                                                                                                       RESULT 4
US-10-683-25-12
US-10-683-25-12
Sequence 12, Application US/10683255
Publication No. US20040063910A1
GENERAL INPORMATION:
APPLICANT: Ravanaugh, William M.
APPLICANT: Ballinger, Marcus
TITLE OF INVENTION: FIREOBLAST GROWTH FACTOR
TITLE OF INVENTION: FIREOBLAST GROWTH FACTOR
TITLE OF INVENTION: FIREOBLAST GROWTH FACTOR
TITLE OF INVENTION: PP01474.101
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: 09/499,846
PRIOR APPLICATION NUMBER: 09/499,846
PRIOR APPLICATION NUMBER: 09/499,846
PRIOR APPLICATION NUMBER: 00/19,002
PRIOR FILING DATE: 1999-02-08
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
95.7%; Score 562; DB 12;
Best Local Similarity 95.5%; Pred. No. 1.2e-49;
Matches 105; Conservative 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-683-255-12
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; ORGANISM: Homo sapiens
US-10-683-255-10
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                              PUBLICATION: OF USE OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: hG-CSF-L-vFc gammal with a 30-amino acid leader peptide (Figure ) OTHER INFORMATION: C) US-09-968-362-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 67, Application US/10071485

| Sequence 67, Application US/10071485
| Publication No. US20030099648A1
| GENERAL INFORMATION:
| APPLICANT: Buyes, Marie-Ange
| APPLICANT: Buyes, Marie-Ange
| TITLE OF INVENTION: Erwin
| TITLE OF INVENTION: GACHEXIA, INMUNE DISEASES AND SKIN DISORDERS
| TITLE OF INVENTION: GACHEXIA, INMUNE DISEASES AND SKIN DISORDERS
| TITLE OF INVENTION: GACHEXIA, INMUNE DISEASES AND SKIN DISORDERS
| TITLE OF INVENTION: GACHEXIA, INMUNE DISEASES AND SKIN DISORDERS
| TITLE OF INVENTION: GACHEXIA, INMUNE WAS CORRENT FILING DATE: 2002-02-07
| FILE REPERBACE: INNS:015
| CURRENT FILING DATE: 2000-02-14
| PRIOR FILING DATE: 1998-08-18
| PRIOR FILING DATE: 1998-06-18
| PRIOR FILING DATE: 1998-06-18
| PRIOR PELICATION NUMBER: EPO 97870122.5
| PRIOR APPLICATION NUMBER: EPO 97870122.5
| PRIOR PELING DATE: 1998-06-18
| WHORE FILING DATE: 1999-08-18
| WHORE FILING DATE: 1997-08-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 APELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTK 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 APPVAGGESVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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Pred. No. 1.6e-50;
1; Mismatches 2; Indels C
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95.7%; Score 562; DB 14; Length 468;
Best Local Similarity 95.5%; Pred. No. 1.1e-49;
Matches 105; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 97.3%;
Matches 107; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
             US20030082679A1
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COTHER INFORMATION: SYNTHETIC
US-10-071-485-67
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US-10-071-485-67
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Gaps

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Indels

Query Match 95.7%; Score 562; DB 14; Best Local Similarity 95.5%; Pred. No. 1.9e-49; Matches 105; Conservative 2; Mismatches 3;

Length 711;

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ASSULTANCE SO, Application US/10071485

Sequence 90, Application US/10071485

Jebblication NO. US2030099948A1

GENERAL INFORMATION:
APPLICANT: Buyee, Marie-Ange
APPLICANT: Buyee, Marie-Ange
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
CURRENT APPLICATION NUMBER: US/10/071,435

CURRENT APPLICATION NUMBER: 09/485,737

PRIOR PAPLICATION NUMBER: PCT/EP 98/05165

PRIOR PELING DATE: 1998-08-14

PRIOR FILING DATE: 1998-06-18

PRIOR PILING DATE: 1998-06-18

PRIOR PILING DATE: 1998-06-18

PRIOR PILING DATE: 1999-06-18

PRIOR PILING DATE: 1997-06-18

PRIOR PILING DATE: 1997-06-18
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PRESEQYNSTYRUVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK 418
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                                                                                                                                                                                                                   Sequence 8, Application US/10683255
; Sequence 8, Application US/10683255
; Publication No. US20040063910A1
; GENERAL INPORMATION:
; APPLICANT: Kavanaugh, William M.
APPLICANT: Ballinger, Marcus
; TITLS OF INVENTION: PIBROBLAST GROWITH FACTOR
; TITLS OF INVENTION: PIBROBLAST GROWITH FACTOR
; TITLS OF INVENTION: PIBROBLAST GROWITH FACTOR
; TITLS OF INVENTION: PROPER: US/10/683,255
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 09/499,846
; PRIOR FILING DATE: 1999-02-08
; PRIOR PILING DATE: 1999-02-08
; NUMBER OF SEQ ID NOS: 12
; SOFTPAARE: SeatSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
US-10-683-255-8
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1 APPVAGGPSVFLFPPKPKDTLMISRTPBVTCVVVDVSHEDPBVKFNWYVDGVEVHNAKTK
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                                                                                                61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                311 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK 360
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US-10-008-063-28

US-10-008-063-28

Sequence 28, Application US/10008063

Sequence 28, Application US/10008063

Sequence 28, Application US/10008063

GENERAL INFORMATION:
APPLICANT: Gross, Jane A.
APPLICANT: Ku, Wenfeng
APPLICANT: Gross, Fancis, J.
TITLB OF INVENTION: Human Tumor Necrosis Factor Receptor
FILE REFERENCE: 00-103

CURRENT FILING DATE: 2001-11-05

NUMBER OF SEQ ID NOS: 46

SOUTHARE: PESESEQ for Windows Version 4.0

SEQ ID NO 28

LENGTH: 232
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| Publication No. US20030092164A1 |
| Publication No. US20030092164A1 |
| GENERAL INFORMATION: |
| APPLICANT: Gross, Jane A. |
| APPLICANT: Ku, Wenfeng M. |
| APPLICANT: Henne, Randal M. |
| APPLICANT: Grant, Prancis, J. |
| TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor FILE REPRENCE: 00-103 |
| CURRENT APPLICATION NUMBER: US/10/008,063 |
| CURRENT FILING DATE: 2001-11-05 |
| NUMBER OF SEQ ID NOS: 46 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 32 |
| INNETH: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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95.1%; Score 558; DB 14;
Best Local Similarity 95.5%; Pred. No. 1.3e-49;
Matches 105; Conservative 0; Mismatches 5;
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ORGANISM: Artificial Sequence
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US-10-008-063-32
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35 APEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPRVKFNWYVDGVEVHNAKTK 94
                                                                    1 APPVAGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                                      61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIBKTISKAK 110
                                                                                                                                                                                       95 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNRALPSSIEKTISKAK 144
Best Local Similarity 95.5
Matches 105; Conservative
                                                                                                                                                                                                                                                                        RESULT 12
US-10-152-363A-33
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                                                                                                                                      16 APEAEGAPSVPLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 APRABGAPSVPLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 94
                                                                                                1 APPVAGGPSVFLFPPKPTLMISRTPBVTCVVVDVSHBDPEVKFNWYVDGVBVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 APPVAGGPSVPLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                   Gaps
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                                                                                                                                                                                       61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                                                                                                               PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAK 125
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         Length 232;
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                                                                                                                                                                                                                                                                                                                                Sequence 35, Application US/10152363A

Publication No. US20030103986A1

GENERAL INFORMATION:

APPLICANT: Rixon, Mark W.

TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins

FILE REPRENCE: 01-20

CURRENT APPLICATION NUMBER: US/10/152,363A

CURRENT PILING DATE: 2002-05-20

FRIOR APPLICATION NUMBER: 60/293,343

PRIOR FILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 70

SOFTWARE: PastSEQ for Windows Version 3.0

LENGTH: 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.1%; Score 558; DB 14; Length 2
95.5%; Pred. No. 1.4e-49;
tive 0; Mismatches 5; Indels
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US-10-15.-363A-31
Sequence 31, Application US/10152363A
Sequence 31, Application US/10152363A
Fublication No. U520030103986AL
GENERAL INFORMATION:
APPLICANT: Rixon, Mark W.
TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
FILE REFERENCE: 01-20
CURRENT APPLICATION NUMBER: US/10/152,363A
CURRENT PILING DATE: 2002-05-20
FRIOR APPLICATION NUMBER: 60/293,343
FRIOR PILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 70
SOFUTARE: PateSEQ for Windows Version 3.0
SEQ ID NO 31
MENTH: 251
       Score 558; DB 14; Length 2
Pred. No. 1.3e-49;
0; Mismatches 5; Indels
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ORGANISM: Artificial Sequence
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       tch
al Similarity 95.5%;
105; Conservative
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Matches 105, Conservative
       Ouery Match
Best Local Similarity
Matches 105; Conserva
                                                                                                                                                                                                                                                                                                  RESULT 10
US-10-152-363A-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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Pred, No. 2e-49;
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; Sequence 42, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.;
; APPLICANT: Xu, Wenfeng
; APPLICANT: Tu, Wenfeng
; APPLICANT: Henne, Randal M.;
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; TITLE OF INVENTION: Human Tumor Necrosis
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILLING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Artificial Sequence
Sequence 33, Application US/10152363A

Sequence 33, Application US/10152363A

Publication No. US200030103966A1

GENERAL INFORMATION:
APPLICANT: Rixon, Mark W.
TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
TITLE APPLICATION NUMBER: US/10/152,363A

CURRENT FILING DATE: 2002-05-20

PRIOR PPLICATION NUMBER: 60/293,343

PRIOR PPLING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 70

SOFTWARE PASSESE for Windows Version 3.0

SEQ ID NO 33

LENDTH: 251
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ORGANISM: Artificial Sequence
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Best Local Similarity
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Gaps

Indels

95.5%; Pred. No. 1.4e-49; tive 0; Mismatches 5;

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95.1%; Score 558; DB 14; Length 344;
Best Local Similarity 95.5%; Pred. No. 2.1e-49;
Matches 105; Conservative 0; Mismatches 5; Indels C
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95.1%; Score 558; DB 14; Length 332;
Best Local Similarity 95.5%; Pred. No. 2e-49;
Matches 105; Conservative 0; Mismatches 5; Indels (
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US-10-152-363A-52
US-10-152-363A-52
Sequence 52, Application US/10152363A
Publication No. US20030103986A1
GENERAL INFORMATION:
APPLICANT: Rixon, Mark W.
ITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
FILE REPERENCE: 01-20
CURRENT FILING DATE: 2002-05-20
PRIOR PILING DATE: 2001-05-34
NUMBER OF SEQ ID NOS: 70
SEQ ID NO 52
LENGTH: 344
                                                                                                                                                                                              RESULT 14
US-10-153-363A-62
| Sequence 62, Application US/10152363A
| Publication No. US20030103986A1
| GENERAL INFORMATION:
| APPLICANT: Rixon, Mark W. |
| APPLICANT: Rixon, Mark W. |
| TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins FILE REPERENCE: 01-20
| FILE REPERENCE: 01-20
| PRIOR PPLICATION NUMBER: US/10/152,363A |
| PRIOR PLILICATION NUMBER: 60/293,343 |
| PRIOR FILING DATE: 2001-05-24 |
| NUMBER OF SEQ ID NOS: 70 |
| SOFURARE: RastSEQ for Windows Version 3.0 |
| LENGTH: 332
 Indels
 'n
 Mismatches
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US-10-152-363A-52
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; OTHER INFORMATION: Fusion protein.
US-10-152-363A-62
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
   105; Conservative
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Search completed: April 29, 2004, 08:55:54 Job time : 39.5 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: April 29, 2004, 08:42:33 ; Search time 16.5 Seconds

(without alignments)

344.173 Million cell updates/sec
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Sequence: 1 APPVAGGPSVFLFPPKPKDT......
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Issued Patents AA:*

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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/pcTuS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/pcTuS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 8, Appli Sequence 90, Appli Sequence 90, Appl
Sections
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Sequence 12, Appl	Seguence 1056, Ap	Sequence 1058, Ap	Sequence 1060, Ap	Sequence 1062, Ap	٠.		Sequence 1066, Ap	Sequence 16, Appl	Sequence 18, Appl	Sequence 33, Appl	Sequence 33, Appl	Sequence 8, Appli	Sequence 10, Appl	Sequence 20, Appl	Sequence 22, Appl	Sequence 4, Appli	Sequence 4, Appli	
US-09-428-082B-12	US-09-428-082B-1056	US-09-428-082B-1058	US-09-428-082B-1060	US-09-428-082B-1062	US-09-428-082B-1070	US-09-428-082B-1064	US-09-428-082B-1066	US-09-428-082B-16	US-09-428-082B-18	US-08-284-391B-33	US-09-218-950-33	US-09-428-082B-8	US-09-428-082B-10	US-09-428-082B-20	US-09-428-082B-22	US-09-178-869-4	US-09-761-413-4	
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28	29	30	31	32	33	34	35	36	37	38	39	40	4	42	43	44	45	

ALIGNMENTS

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GENERAL INFORMATION:

APPLICANT: Buyse, Marie-Ange
APPLICANT: Buyse, Marie-Ange
APPLICANT: Buyse, Marie-Ange
TITLE OF INVENTION: Erwin
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
TITLE OF INVENTION: UNDERSION CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
CURRENT FILLOR DATE: 1996-08-14
PRIOR PELICATION NUMBER: EPO 98970139.7
PRIOR PELING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: EPO 9770122.5
PRIOR APPLICATION NUMBER: EPO 9770122.5
PRIOR APPLICATION NUMBER: EPO 9770122.5
PRIOR PILLOR DATE: 1997-08-18
PRIOR FILLOR DATE: 1997-08-18
PRIOR FILLOR DATE: 1997-08-18
INVERSE OF SEQ ID NOS: 104
SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NO 67
HENGHH, 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
US-09-499-846-12
Sequence 12, Application US/09499846
Fatent No. 6656728
GENERAL INFORMATION:
TITLE OF INVENTION: FIRROBLAST GROWTH FACTOR
TITLE OF INVENTION: FIRROBLAST GROWTH FACTOR
TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION
FILE REFERENCE: 035784/195012 (5784-
                     Sequence 67, Application US/09485737B Patent No. 6350860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-09-485-737B-67
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                                                                                                                                                                                                        Length 488;
                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-09-499-846-10
Sequence 10, Application US/09499846
Patent No. 6656728
GENERAL INFORMATION:
APPLICANT: Kavanaugh et al.
TITLE OF INVENTION: FIRROBLAST GROWTH FACTOR
TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION
FILE REFERENCE: 035784/195012 (5784-
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 497
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US-09-499-846-8

Sequence 8, Application US/09499846

Patent No. 6656728

GENERAL INFORMATION:
APPLICANT: Ravanaugh et al.
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION
FILE REFERRINCE: 0357084/195012 (5784-
CURRENT APLICATION NUMBER: US/09/499,846
CURRENT FILING DATE: 2000-02-07

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 525
                                                                                                                                                                                                    Query Match
95.7%; Score 562; DB 4;
Best Local Similarity 95.5%; Pred. No. 2.8e-58;
Matches 105; Conservative 2; Mismatches 3;
CURRENT APPLICATION NUMBER: US/09/499,846
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 12
SEQTWARE: EastSEQ for Windows Version 3.0
LENGTH: 488
                                                                                                                   TYPE: PRT; ORGANISM: Homo sapiens
US-09-499-846-12
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ORGANISM: Homo sapiens
US-09-499-846-8
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DS-9485-7418-70

Sequence 90, Application US/09485737B

Patent No. 6350860

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE REFERENCE: INNS:015

CURRENT FILING DATE: 1999-08-14

PRIOR APPLICATION NUMBER: BC/09/485,737B

CURRENT FILING DATE: 1999-08-14

PRIOR APPLICATION NUMBER: BC/09/6165

PRIOR APPLICATION NUMBER: BC/09/6165

PRIOR APPLICATION NUMBER: BC/09870139.7

PRIOR APPLICATION NUMBER: BC/09/618

PRIOR PILING DATE: 1998-06-18

PRIOR PILING DATE: 1998-06-18

PRIOR PILING DATE: 1997-08-18

NUMBER OF SC/10 NOS: 104

SC/10 NO 96

LENGTH: 111
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                                                                                                                    1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                           Gaps
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   Length 525
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Sequence 62, Application US/09746359A

GENERAL INFORMATION:

APPLICANT: Thompson, Penny

APPLICANT: Ku, Wenfeng

APPLICANT: Kelly, James D.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Bagan, Maribeth A.

APPLICANT: Bagan, Maribeth A.

APPLICANT: Bagers, Stephen R.

APPLICANT: Chandrasekher, Yasmin A.

APPLICANT: PREFERENCE: 99-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 95.7%; Score 562; DB 4;
Best Local Similarity 95.5%; Pred. No. 4.7e-58;
Matches 105; Conservative 2; Mismatches 3;
Query Match 95.7%; Score 562; DB 4; Best Local Similarity 95.5%; Pred. No. 3.1e-58; Matches 105; Conservative 2; Mismatches 3
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US-09-485-737B-90
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Sequence 21, Application US/08444644

Batent No. 6015555
GENERAL INFORMATION:
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                343 APEAEGAPSVFLPPPKFKDTLMISRTPEVTCVVVDVSHEDDEVKENWYVDGVENHNAKTK 402
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95.1%; Score 550; DB 4; Length 559;
Best Local Similarity 95.5%; Pred. No. 1e-57;
Matches 105; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Foster, Donald C.
APPLICANT: Roster, Donald C.
APPLICANT: Ru, Wenfeng
APPLICANT: Ru, Wenfeng
APPLICANT: Rally, James D.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Bagan, Maribeth A.
APPLICANT: No. 66102864k, Julia E.
APPLICANT: SPOIN NUMBER: 60/213, 341
PRIOR FILING DATE: 2000-66-22
NUMBER OF SEQ ID NOS: 72
ANDRER PARICE FASTERQ for Windows Version 3.0
APPLICANT: SPOIN NO. 231
APPLICANT NO. 231
APPLI
CURRENT APPLICATION NUMBER: US/09/146,359A
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/171,969
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1000-06-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 62
TENGTH: 559
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23, Application US/09746359A Patent No. 6610286 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORGANISM: Homo sapiens
US-09-746-359A-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-746-359A-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 APELLGGPSVFLFPPFKPKDTLMISRTPEVTCVVVDVSHBDPEVKFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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AUDKESSEE: Hamiltia Drive
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
COUNTRY: USA
ZIP: 02173
COMPUTER READBLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE: US/08/44,644
FILING DATE: US/08/444,644
PRIOR APPLICATION DATE: US/08/444,644
PRIOR APPLICATION DATE: US/08/444,644
PRIOR APPLICATION DATE: US/08/444,644
PRIOR APPLICATION DATE: US/08/444,646
PRIOR APPLICATION DATE: US/08/232,246
PR
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TRANSFERRIN RECEPTOR SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 94.5%; Pred. No. 1.5e-58;
Matches 104; Conservative 2; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
US-08-232-246A-21
Sequence 21, Application US/08232246A
FORTER ON 632950B
GENERAL INFORMATION:
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 110 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-444-644-21
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378 APEAEGAPSVFLFPPKPKDYTAMISKIPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 437

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RESULT

1 APPVAGGESVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK

Score 558; DB 4; Length 594; Pred. No. 1.1e-57; 0; Mismatches 5; Indelb

Query Match
Best Local Similarity 95.5%;
Matches 105; Conservative

; TYPE: PRT ; ORGANISM: Homo sapiens US-09-746-359A-23

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6 APELLGGESVFLFPPKDTLMISRIPSVTCVVVDVSHBDPSVKFNMYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 APPVAGGPSVFLFPPKDKDTLMISRTPBVTCVVVDVSHBDPEVKFNWYVDGVBVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 PREEQINSTYRVVSVLTVLHQDMLNGKEYKCKVSNRALPAPIBKTISKAK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                             COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,539D
FILING DATE: 21-Apr-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/178583
FILING DATE: 07-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/178583
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT TRORMATION:
NAME: SYODOGA, CTA19 G.
REGISTRATION NUMBER: 39,044
REFREENCR/POCKET NUMBER: 39,044
REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 39,044
REPREENCR/POCKET NUMBER: 39,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 116 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-232-539D-55
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONUTGATES
NUMBERS OF SEQUENCES: 46
CORRESPONDENCES AGENT OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
STATE: Town Militia Drive
CITY: Learning on State of Sequences and CITY: Learning on State of Sequences and CITY: Learning on State of Sequences and CITY: Learning on Sequences and CITY: Learning on Sequences and CONGRESS: Seq
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RESULT 11
US-08-430-633-4
US-08-430-63-4
US-08-4

RESULT 10
US-08-232-539D-55
Sequence 55, Application US/08232539D
Sequence 55, Application US/08232539D
Patent No. 5965709
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: 19E Antagonists
NUMBER OF ENGENTES: 60
CORRESPONDENCE ADDRESS:
ADDRESSE: Genertech, Inc.
STREET: 1 NMA Way
CITY: South San Francisco
STATE: California
CONTRY: USA
ZIP: 94080

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60
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US-08-620-694A-4
Sequence 4, Application US/08620694A
Sequence 4, Application US/08620694A
Sequence 4, Application US/08620694A
Sequence 4, Application US/08620694A
Sequence 4, Application Seguence 3, Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.9%; Score 557; DB 1; Length 212; 94.5%; Pred. No. 3.6e-58; tive 2; Mismatches 4; Indels
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STREET: 51 University Street
CITY: Seattle
STATE: WAS
COUNTRY: WAS
COUNTRY: WAS
COUNTRY: WAS
COUNTRY: BAD10
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER RADDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694A
FILING DATE: 21 MARCH 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION NUMBER: USSN 08/410,535
RICHASIFICATION NUMBER: USSN 08/410,535
RICHASIFICATION NUMBER: USSN 08/410,535
RICHASIFICATION NUMBER: USSN 08/410,535
RICHASIFICATION NUMBER: 33 MARCH 1995
CLASSIFICATION NUMBER: 33 MARCH 1995
CLASSIFICATION NUMBER: 34,695
REFERENCE POCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: 08/235,397
FILING DATE: 04/28/94
ATTORNEY/AGENT INFORMATION:
NAME: PERKING, PALTICIA A.
REGISTRATION NUMBER: 34/693
REFERENCE/DOCKET NUMBER: 2612
TELEPRONE: (206) 23-0644
INFORMATION: (206) 23-0644
INFORMATION: (206) 23-0644
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: APPLOYEC:
ONGRANISM: Human
INMEDIATE SOURCE:
ONGRANISM: Human
INMEDIATE SOURCE:
CLONE: 19G1 FC
US-08-430-633-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 94.5'
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC
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THERPORE, (206)

THERPORE, (206)

THERPORE CASACTRETRICS

THE CASACTRE
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CLONE:
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1 APPVAGGPSVPLPPPXPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 60 14 APELLGGPSVFLFPFRENDTLMISKTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 73 0; Gaps 61 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110 Length 212; 4; Indels Query Match

94.9%; Score 557; DB 3;

Best Local Similarity 94.5%; Pred. No. 3.6e-58;

Matches 104; Conservative 2; Mismatches 4; 셤 ઠે

Query Match 94.9%; Score 557; DB 2; Length 212; Best Local Similarity 94.5%; Pred. No. 3.6e-58; Matches 104; Conservative 2; Mismatches 4; Indels

TYPE: anino acid

TOPDLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

ORGANISM: Human

INMEDIATE SOURCE:

CLONE: IgG1 Fc
US-08-936-854-4

8

RESULT 15
US-09-022-696-4
IS-09-022-696-4
Sequence 4, Application US/09022696
Fatent No. 6072037
Fatent No. 6072037
SENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, Malliam
TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADORESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA 74 PREEQINSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 123 g

US-09-022-255-4

US-09-022-255-4

Sequence 4, Application US/09022255

Sequence 4 Application US/09022255

Sequence 4 Application US/09022255

PAPLICANT: Yao, Zhengbin

APPLICANT: Spriggs, Melanie

APPLICANT: Panslow, William

TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSE:

ADDRESSE:

CORRESPONDENCE ADDRESS:

CORRESPONDE

COMPUTER READBLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,696
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE: 34.695
FILING DATE: 21 WARCH 1995
CLASSIFICATION:
APPLICATION NUMBER: 34,695
FILING DATE: 34,695
FILING DATE: 24 WARCH 1995
FILING DATE: 24 WARCH 1995
FILING DATE: 24 WARCH 1995
FILING DATE: 25 WARCH 1995
FILING DATE: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELLEPHONE: (206)597-0430
FILIEPHONE: (206)597-0430
FILIEPHONE: (206)597-0430
FILIEPHONE: (206)597-0430
FILIEPHONE: (206)597-0430
FILIEPHONE: APPLICATION INFORMATION:
FERRENCE CHARACTERISTICS:
FERRENCE CHARACTERISTICS:

COMPUTER READBABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:

98101

PELLING DATE:
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 23 MARCH 1995
ATTONEY/ABOTY INPORMATION:
NAME: PERKENEY 23 MARCH 1995
FEBREMENEY DOCKET NUMBER: 34,695
FEBREMONEY DOCKET NUMBER: 2617-B
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION ON: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant

TOPOLOGY: linear MOLECULE TYPE: protein ORIGINAL SOURCE: ORGANISM: Human IMMEDIATE SOURCE:

TYPE: amino acid STRANDEDNESS: not relevant 212 amino acids TOPOLOGY: linear MOLECULE TYPE: protein ORIGINAL SOURCE: LENGTH:

ORGANISM: Human IMMEDIATE SOURCE: CLONE: IGG1 FC

ö Query Match

94.9%; Score 557; DB 3; Length 212;
Best Local Similarity 94.5%; Pred. No. 3.6e-58;
Matches 104; Conservative 2; Mismatches 4; Indels

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; US-09-022-255-4

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Search completed: April 29, 2004, 08:47:43 Job time : 17.5 secs

1.

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

April 29, 2004, 08:41:33 , Search time 13.5 Seconds (without alignments) 783.783 Million cell updates/sec Run on:

US-09-674-857-12 583 1 APPVAGGPSVFLFPPKPVDT......CKVSNKGLFSSIBKTISKAK 110

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	gamma-4 chain	g gamma-2 chain	g gamma chain C	7	g gamma-1 chain	g heavy chain V	g gamma-3 chain	g gamma-3	g gamma-3 h	g gamma 2b	g gamma 2a	g gamma 4	g gamma 3	g gamma 1 chai	g heavy	g gamma cha	g gamma-2b	g gamma-	g heavy ch	g gamma-2 chai	g gamma-3	g gamma-3	g gamma-2	g gamma-1	g gamma-1	onoclonal a	датта-2с	g gamma-2b	ы
SUMMARIES	ID	G4HU	G2HU	PT0207	531866	GHHU	869339	A60764	A23511	G3HUWI	147160	147159	147162	147161	147158	C30554	GHRB	PS0018	831459	S220B0	G2GP	Gamsc	G3MSM	806611	GIMS	GIMSM	PC4436	S00847	GZMSBM	GZMS11
	DB DB	-	-1	~	4,	н	~	Ċ	N	H	7	ď	(7)	Ň	(7	(7	Н	~	N	N	Н	Н	-1	N	н	M	N	N	H	-
	Length	327	326	234	255	330						328	277	328	328	308	323	333	472	470	329	329	398	327	324	393	444	329	405	474
æ	Query Match	96.9	m.	ci	92.8	92.8	a	П	П	æ,	0	0	đ١	76.0	9	74.3	74.3	74.3	74.3	73.9	73.1	71.5		•		ο.	9.	69.1	68.4	68.4
	Score	ı	542.5	541	541	541	541	531	531	518	470	470	465	443	443	433	433	433	433	431	426	417	417	409	405	405	405	403	399	399
	Result No.		C)	m	4	w	9	7	σο	σ	10	11	12			15		17	₽		20		22	23	24	. 25	26	27	28	53

Ig gamma-2a chain		U	gamma-2a	Ig gamma-1 chain C	Ig gamma-2b chain	Ig gamma-2a chain	gamma-2a	-		gamm	Ig epsilon-chain -	epsilon	Ig gamma-1 chain C	heavy chain	Ig epsilon chain C
G2MSAB	G2MSA	G2MSAM	537483	PS0017	S01321	S40295	PS0019	B30503	A30503	I46732	136948	BHHU	S14236	\$04845	EHRT
٦	H	Н	~	N	N	Ŋ	N	N	N	N	N	H	~	N	-
335	330	399	469	326	475	446	322	112	88	180	426	423	152	549	429
67.9	67.4	67.4	67.4	66.7	66.0	65.7	58.8	53.3	47.7	44.3	28.7	28.6	28.3	26.4	25.9
396	393	393	393	389	385	383	343	311	278	258	167.5	166.5	165	154	151
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Query Match 96.9%; Score 565; DB 1; Length 327; Best Local Similarity 97.3%; Pred. No. 1.2e-48; Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0; Qy	C; Keywords: duplication; glycoprotein; heteroetramer; immunoglobulin F;20-85/Oomain: immunoglobulin homology <im1> F;20-85/Oomain: immunoglobulin homology <im2> F;34-203/Domain: immunoglobulin homology <im3> F;240-307/Domain: immunoglobulin homology <im3> F;240-307/Domain: immunoglobulin homology <im3> F;240-307/Domain: immunoglobulin homology <im3> F;240-307/Domain: immunoglobulin homology (IM3) F;240-307/Domain: immunoglobulin homology (IM3) F;240-307/Domain: immunoglobulin homology (IM3) F;270-83,141-201,247-305/Disulfide bonds: #status predicted F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted</im3></im3></im3></im3></im2></im1>	A;Molecule type: DNA A;Residues: 1-327 < RELL> A,Residues: 1-327 < RELL> A,Note: the sequence agedence agedence of the germline gene A,Note: the sequence agedence of the Constant R;bink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C. B;ochem. J. 117, 33-47, 1970 A;Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant A;Reference number: A90249; MUID:70207560; PMID:4192699 A;Accession: A90249 A;Molecule type: protein A;Residues: 1-30;81-326 < PIN>	RESULT 1 G4HU Ig gamma-4 chain C region - human C;Species: Homo sapiens (man) C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999 C;Accession: A90933, A90249; A02150 R;Ellison, J.; Buxbaum, J.; Hood, L. DNA 1, 11-18, 1981 A,Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene. A;Reference number: A90933; WUID:83157104; PMID:6299662	
Infilition by the control of the con	figure described Extracts in Pour cases, such as 197 and 197 a		e germline gene M.; Milstein, C. Partial amino acid sequence of the PMID:4192699	pr-1982 #text_change 16-Jul-1999 unoglobulin C-gamma4 gene. PMID:6299662 e germline gene M.; Milstein, C. Partial amino acid sequence of the PMID:4192699

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RESULT 2

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A,Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C,Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C,Accession: S31866
R,Filpula, D.
submitted to the EMBL Data Library, February 1993
A,Bestription: Sorceing method for protein-protein interactions of cloned gene products
A,Reference number: S31866
                                                                                                                                                                    111 APPVA-GPSVPLFPPKPXDTIMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTK 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 APPVAGGESVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                       Ig gamma chain C region - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Species: Pan troglodytes (chimpanzee)
C;Bate: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C;Accession: PT0207
R;Ehrlich, P.H; Moustafa, Z.A.; Oestberg, I.
Mol. Immunol. 28, 319-322, 1991
A;Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A;Reference number: PT0207; MUID:91287716; PMID:2062315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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   Length 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-234 <EER>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Superfamily: immunoglobulin
C;Keywords: immunoglobulin
F;48-117/Domain: immunoglobulin homology <IMM>
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Pred. No. 2.2e-46;
4; Mismatches 5;
      DB 1;
Score 542.5; DB 1
Pred. No. 2.1e-46;
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Pred. No. 2e-46;
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                                                            3; Mismatches
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         93.18;
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Best Local Similarity 91.8%;
Matches 101; Conservative
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Best Local Similarity 91.8
Matches 101; Conservative
                                                               Conservative
         Query Match
Best Local Similarity
Matches 103; Conserv
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A; Residues: 1-255 <FIL>
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                                                                        ig gamma-2 chain C region - human Cigemea-2 chain C region - human Cigemea-2 chain C region - human Cigemeies: Homo sapidens (man) C;Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 21-Jul-2000 C;Date: 30-Apr-1981 #sequence revision 13-Jun-1981 #sezion G;Accession: A93906; A92809; A93132; A93132; A02148 R;Ellison, J.; Hood, L. Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982 A;Tile: Linkage and sequence homology of two human immunoglobulin gamma heavy A;Reference number: A93906; MUID:82197621; PMID:6804948
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Cycomplex: An immunoglobulin heterotetramer subunit consists of two identical light (ka hain disulfide bonds In some cases, such as 1gA and 1gM, the subunits associate into l hain disulfide bonds In some cases, such as 1gA and 1gM, the subunits associate into l (s. Superfamily: immunoglobulin c region; immunoglobulin homology (Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin homology (MIN) F:137-206.Domain: immunoglobulin homology (MIN) F:243-310/Domain: immunoglobulin homology (MIN) F:27-83,144-204,250-308/Disulfide bonds: #status experimental F:103/Disulfide bonds: interchain (to heavy chain) #status experimental F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
                                                                                                                                                                     of monoclonal IgG1 immunoglo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92.8%; Score 541; DB 1; Length 330; 91.8%; Pred. No. 3e-46; tive 4; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: armotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
HOppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure cempromide cleavage produces, and the disulfide bridges.
A;Reference number: A91667; WUID:77070567; PMID:1002129
A;Contents: annotation; disulfide bonds
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Pred. No. 3.5e-46;
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R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
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91.8%; Pred. No. 3....
4; Mismatches
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C;Species: Homo sapiens (man)
C;Date: 31-Dec.1979; Ascquence revision 23-Oct-1981 #text_change 16-Jul-1999
C;Accession: A09442, A32219; A80198; A33915; A02149
C;Accession: B.; Rosenwasser, B.; Prelli, P.; Franklin, B.C.
B;Cachmistry 19, 4304-4308, 1980
A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy
A;Teference number: A90442; MID181021848; PMID1674747
A;Contents: heavy chain disease protein Wis
A;Residues: 1-289 KRA>
A;Residues 1-289 KRA>
A;Note: this protein lacks most of the V region and all of the CH1 region. Residue 12
A;Note: the sequence of residues 42-76 was taken from the reference that follows
A;Reference number: A9219; MID17118561; PMID140263
A;Note: the sequence of residues 42-76 was taken from the reference that follows
A;Reference number: A9219; MID177118561; PMID140263
A;Reference number: A9219; MID177118561; PMID140263
A;Residues: 12-97 kMID2-7118561; PMID1402263
A;Residues: 12-97 kMID2-7118561; PMID1402263
A;Residues: 12-97 kMID2-7118561; PMID1402263
A;Note: Cystelnes at protein
A;Residues: 12-97 kMID2-7118561; PMID180263
A;Note: Cystelnes at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inte A;Note: Cystelnes at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inte A;Note: Cystelnes at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inte A;Note: Cystelnes at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inte A;Note: Cystelnes at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inte A;Note: Cystelnes at positions 24, 27, 31, 39, 42, 48, 54, 57, 63, 69, and 72 form inte A;Note: Cystelnes at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inte A;Note: Cystelnes at Positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inte A;Note: Cystelnes at Positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inte A;Note: Cystelnes at Positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inte A;Note: Cystelnes at Positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, 
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A;Residues: 59-125, EBB, 128-226, 228-289 <WOL>
A;Note: this protein lacks most of the V region, all of the CH1 region, and part of the A;Note: this protein lacks most of the V region, all of the CH1 region, E.C.; Hood, L. Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A;Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion A;Reference number: A93915; MUID:82247835; PMID:6808505
A;Contents: heavy chain disease protein Omm
A;Accession: A93915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156-15
A; Note: a carboxy1-terminal Lys is removed posttranslationally
A; Note: this sequence may represent an allelic form or another gamma chain subclass
C; Comment: The heavy chain disease protein Wis is shown.
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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19 gamma 2b chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 APELLGGPSVPLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVQVHNAKTK
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A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin C region; immunoglobulin; pyroglutamic acid C;Superfamily: immunoglobulin; pyroglutamic acid F;203-270/Domain: immunoglobulin homology <IMM>F;203-270/Domain: immunoglobulin homology <IMM>F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PREEDFINSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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88.9%; Score 518; DB 1;
Best Local Similarity 87.3%; Pred. No. 5e-44;
Matches 96; Conservative 7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
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19 gamma-3 chain C region (allotype G3m(b)) - human
CSpecies: Homo sapiens (man)
CSpecies: Homo sapiens (man)
CSPecies: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Date: 28-Dec-1987 #sequence C, Trawford, D.H.; Defranc, M.P.; Defranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: A;Reference number: A25511; MiJD:86148807; PMID:3081877
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A; Residues: 1-377 < HUC>
A; Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C; Genetics: A; Genetics: GDB:119339; OMIM:147120
                                                                                                                                                                       AG0764

Ig gamma-3 chain C region, form LAT - human
CjSpecies: Homo sapiens (man)
CjSpecies: Homo sapiens (man)
CjSpecies: Homo sapiens (man)
CjSpecies: Homo sapiens (man)
CjSpecies: Lefranc, May-1993 #text_change 16-Jul-1999
CjAccession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (GmbO, bl, c3, c5, u) with an IGHG4
A;Reference number: A60764; MuID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 cHUC>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Reywords: immunoglobulin homology < IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 APPVAGGPSVFLFPPKEDTLMISRIPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
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PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110

61 221

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Length 377;

Score 531; DB 2; Length 37 Pred. No. 3.5e-45; 4; Mismatches 7; Indels

Query Match 91.1%; Best Local Similarity 90.0%; Matches 99; Conservative

PREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 270

PREEQFINSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110

61

g 8 Ig gamma-3 heavy chain disease proteins

RESULT 9 G3HUWI

Length 377;

91.1%; Score 531; DB 2; Length 37 larity 90.0%; Pred. No. 3.5e-45; Conservative 4; Mismatches 7; Indels

Local Similarity nes 99, Conserv

Query Match

A,Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglabulin C region; immunoglabulin homology
C;Keywords: immunoglabulin
F;20-85/Domain: immunoglabulin homology <IMM>

707.77-/00-4/0-60-80

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Gaps

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igramma 1 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47158
R;Kacskovics, I.; Sun, J.; Butler, J.E.
R;Kacskovics, I.; Sun, J.; Butler, J.E.
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Reference number: I47158; MUID:95015845; PMID:7930579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gramma 3 chain constant region - pig (fragment)
C,Species: Sus scrcfa domestica (domestic pig)
C,Species: Sus scrcfa domestica (domestic pig)
C,Accession: 147161
R,Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A,Titler: Five putative subclasses of swine IgG identified from the cDNA sequences of A,Reference number: 147158; MUD:95015845; PMID:7930579
A,Accession: I47161
A,Molecule type: MRNA
A,Residues: 1-328 cKAC>
A,Conserved to MD:9433127; PIDN:AAA52219.1; PID:9433128
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                                                                                                                                                                                                                                                                                                                                                                            65 GPSARIFPPREKDTLMLSRTPKVTCVVDVSQENPEVQFSWTVDGVEVHTAQTREKEEQF 124
                                                                                                                                                                                                                                                                                                                                          7 GPSVFLFPPKFKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF 66
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A;Nolecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122
C;Genetics:
A,Molecule type: mRNA
A,Residues: 1-277 <KAC>
A,Residues: 1-277 <KAC>
C,Genetics: EMBL:U03782; NID:g433129; PIDN:AAAS2220.1; PID:g433130
C,Genetics:
A,Gene: IGG
A,Gene: IGG
C,Superfamily: immunoglobulin C region; immunoglobulin homology
P,82-151/Domain: immunoglobulin homology <IPM>
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                                                                                                                                                                                                                            Length 277;
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
P;133-202/Domain: immunoglobulin homology <IMM>
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F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 NSTYRVVSVLTVLHQDWLNGKBYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.0%; Score 443; DB 2; Length 32 78.6%; Pred. No. 1.7e-36; Live 12; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.8%; Score 465; DB 2;
80.8%; Pred. No. 8.9e-39;
iive 12; Mismatches B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 78,6%
Warches 81; Conservative
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.8%
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
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147159
Ig gamma 2a chain constant region - pig (fragment)
G.Species: Sus scrofa domestica (domestic pig)
G.Species: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
G.Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
G.Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
G.Batesokovics, I.; Sun, J.; Butler, J.E.
J. Immunol: 153, 3565-3573, 1994
A.Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a A.Accession: 147159
A.Accession: 147159
A.Accession: 147159
A.Holecule type: m2NA
A.Residues: 1-328 <KAC>
A.Accession: references: EMBL:U03779; NID:9433123; PIDN:AAA52217.1; PID:9433124
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   C;Accession: 147160
R;Kacsexvics, 1.; Sutler, J.E.
J. Immunol. 153, 3565-3573, 1994
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Accession: 147160
A;Recence number: 147158; MUID:95015845; PMID:7930579
A;Accession: 147160
A;Status: preliminary: translated from GB/EMBL/DD3J
A;Residues: 1799: mRMA
A;Residues: 1-328 «KAC-
A;Cross-references: EMBL:U03780; NID:9433125; PIDN:AAA52218.1; PID:9433126
C;Genetics: A;Gene: IgG2b
C;Genetics: A;Gene: IgG2b
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology
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147162
167162
16 gamma 4 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: 147162
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Datession: 147162
B;Xacskovics, I.; Sun, J.; Butler, J.B.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Teterence number: 147158; MUID:95015845; PMID:7930579
A;Steference number: translated from GB/EMBL/DDBJ
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A;Gene: 1963a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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ö 7 GPSVFLFPPKPKDTLMISRTPBVTCVVVDVSQEDPBVQFNWY/DGVEVHNAKTKPREEQP 66 Gaps ö Query Match 76.0%; Score 443; DB 2; Length 328; Best Local Similarity 78.6%; Pred. No. 1.7e-36; Matches 81; Conservative 12; Mismatches 10; Indels d 8 g

RESULT 15
C30554
Ig heavy chain C region - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000
C;Accession: C30554
R;Folley, R.C.; Beh, K.J.
J: Immunol: 142, 708-711, 1989
A;Title: Isolation and sequence of sheep Ig H and L chain cDNA.
A;Reference number: A30554; MUID:89093962; PMID:2492052
A;Accession: C30554
A;Accession: C30554
A;Accession: C30554
A;Accession: C30554
A;Molecule type: mRNA
A;Residues: 1-308 <FOL>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;113-182/Domain: immunoglobulin homology <IMM>

Query Match 74.3%; Score 433; DB 2; Length 308; Best Local Similarity 71.6%; Pred. No. 1.5e-35; Matches 78; Conservative 13; Mismatches 18; Indels

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Search completed: April 29, 2004, 08:46:58 Job time : 14.5 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

April 29, 2004, 08:37:47 ; Search time 10 Seconds (without alignments) 572.772 Million cell updates/sec Run on:

US-09-674-857-12 583 1 APPVAGGPSVFLFPPKFKDT......CKVSNKGLPSSIEKTISKAK 110 Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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Krawlinkel U., Rabbitts T.H.;
"Comparison of the hinge-coding segments in human immunoglobulin gamma
heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
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MEDLINE-80001357; PubMed=113060;
Connell G.E., Parr D.M., Hofmann T.;
"The amino acid sequences of the three heavy chain constant region domains of a human 1962 myeloma protein.";
Can. J. Biochem. 57:758-767(1979).
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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MEDLINE=82197621; PubMed=6804948;
Blison J.W., Hood L.E.;
"Linkage and sequence honology of two human immunoglobulin gamma heavy chain constant region genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
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MEDLINE=83001943; PubMed=6811139;
MEDLINE=83001943; PubMed=6811139;
Takabashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
"Structure of human immunoglobulin gamma genes: implications for evolution of a gene family.";
Cell 29:671-679(1982).
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                                                                                                                                                                                                                  96.9%; Score 565; DB 1; Length 327; 97.3%; Pred. No. 1.3e-50; ive 0; Mismatches 3; Indels
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16-OCT-2001 (Rel. 40, Last annotation update)
19 gamma-2 chain C region.
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Matches 107; Conservative
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EMBO J. 1:403-407(1982).
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This SWISS-TROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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S -> A (IN MYSLOMA PROTEINS TIL & ZIE).

C -> A (IN REF. 3).

C -> S (IN REF. 3).
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                                                                                                                                                                                                                                                   Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri "Characterization of the two unique human anti-flavin monoclonal
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Francione B., Milstein C., Pink J.R.L.;
"Structural studies of immunoglobulin G.";
Nature 221:145-148(1969).
                                                                                                                                                                                                                                                                                             immunoglobulins.";
Eur. J. Biochem. 228:886-893(1995)
                                                                                                                                                                                                             SEQUENCE OF 1-121 (DOT).
MEDLINE-95255298; PubMed=7737190;
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MEDINE-80114419; PubMed=118920; Hofmann T., Parr D.M.; "A note of the amino acid sequence of residues 381-391 of human immunoglobulins gamma chains."; Mol. Immunol. 16:923-925(1979).

SEQUENCE OF 238-275 (ZIE)

REVISIONS TO 25, 59, 60 AND 264-268 (ZIE). Hofmann T., Parr D.M.; Submitted (MAR-1980) to the PIR data bank.

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us-09-674-857-12.rsp

DISULFIDE BONDS

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SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
MEDLINE=71064024; PubMed=5489771;
Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
Waxdal M.J., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. VII. Amino
"The sequence of basy-chain cyanogen bromide fragments H1-E4.";
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                        [4]

**SEQUENCE** (MYELOMA PROTEIN NIE).**

**MEDLINE=77070269; PubMed=826475;

**Ponsting1 H., Hilschmann N.;

**The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.", Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The covalent structure of a human gamma G-irmunoglobulin. 8. acid sequence of heavy-chain cyanogen bromide fragments H5-H7. Biochemistry 9:3171-3181(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFIDE BONDS.
MEDINE=71064027; PubMed=4923144;
MEDINE=71064027; PubMed=4923144;
Gall W.E., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. X.
Intrachain disulfide bonds.";
Intrachain disulfide bonds.";
[7]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-71064025, PubMed-5530842,
Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
DB 1; Length 326;
                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS. MEDLINE-83289131; PubMed-6884994;
                                                              3
93.1%; Score 542.5; DB 1
93.6%; Pred. No. 2.7e-48;
iive 3; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCI HUMAN STANDARD; PRT; 330 AA. P01857-1 JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) 1G gamma-1 chain C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=82274238; PubMed=6287432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 136-329 (EU).
                                                                 Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Edelman G.M.;
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GCI HUMAN

GCI HUMAN

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                                                                                                                        "Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus aureus at 2.9- and 2.8-A resolution."; Biochemistry 20:231-2370(1981).

-! MISCELLANBOUS: Nie has the GIM(17) allotypic marker, 97-K, and the GIM(1) markers, 239-D and 241-L. KOL and EU sequences have the GIM(1) marker and the GIM (non-1) markers.

-! MISCELLANBOUS: Nie also differs in the amidation states of 15, 116, 198, 269 and 272.

-! MISCELLANBOUS: EU also differs in the amidation states of 155, 166, 177, 195, 199, 269, and 272 and in the order of residues 269-272.
               Dreker L., Schwarz J., Reichel W., Hilschmann N.; Ribard antibody structure. The primary structure of a monoclonal lgg1 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the i- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges."; Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
                                                                                                                                                                                                                                                                                                                                                                                                               -!- MISCELLANBOUS: KOL also differs in the amidation states of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERCHAIN (WITH LIGHT CHAIN) .
                                                                                             X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
MEDLINE-81208100; PubMed=7236608;
Deisenhofer J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CH1.
HINGE.
CH2.
CH3.
                                                                                                                                                                                                                                                                                                                                                                                          J00228; AAC82527.1; ALT_INIT
                                                                                                                                                                                                                                                                                 residues 198, 267 and 272.
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110
223
330
83
103
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        MEDLINE=77070267;
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224
227
103
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DOMAIN
DOMAIN
DOMAIN
DOMAIN
DISULPID
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us-09-674-857-12.rsp

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MEDLINE=82247635; PubMed=6808505;
MEDLINE=82247635; PubMed=6808505;
MEDLINE=82247635; PubMed=6808505;
MEDLINE=82247635; PubMed=6808505;
Franklin B.C. Hood L., Barritault D., Frangione B.,
Gamma Heavy chain disease in man: cDNA sequence supports partial
gene deletion model.";
Proc. Natl. Acad. Sci.,
Proc. Natl. Acad. Sci.,
I.- SUBGNIT: Dimer linked by 12 disulfide bonds; it has an extra
innerchain disulfide bond at position 7 in addition to the 11
normally present in the hinge region.
I. MISCELLANEOUS: The heavy chain disease protein WIS is shown.
I. MISCELLANEOUS: The sequence of residues 42-76 was taken from the
                Frangione B., Rosenwasser E., Prelli F., Franklin B.C.; "Primary structure of human gamma 3 immunoglobulin deletion mutant: gamma 3 heavy-chain disease protein Wis."; Biochemistry 19:4304-4308 (1980).
                                                          REVISIONS TO 12-97 (PROTEIN WIS).
MEDLINE=77118561; PubMed=402363;
Michaelsen T.E., Frangione B., Franklin E.C.;
Wichaelsen T.E., Frangione B., Franklin E.C.;
Whichaelsen T.B., Prangione B., Franklin E.C.;
Wichaelsen T.B., Frangione B., Franklin E.C.;
Jeptin Station of a 15-amino acid residue basic unit.";
J. Biol. Chem. 252:883-889(1977).
                                                                                                                            MEDILINE-77021516; PubMed=82395; MRDILINE-77021516; PubMed=82395; MROIfenstein-Todel C., Francione B., Prelli F., Franklin B.C.; The amino acid sequence of 'heavy chain disease' protein ZUC. Structure of the Fc fragment of immunoglobulin G3."; Biochem, Biophys. Res. Commun. 71:907-914(1976).
                                                                                                                       REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC).
SEQUENCE (DISEASE PROTEIN WIS)
MEDLINE=81021548; PubMed=67747
     N-LINKED (GLCNAC. ..).
REMOVED POST-TRANSLATIONALLY.
K -> R (IN GIM(3) MARKER).
/FTIA-VAR 003886.
D -> E (IM GIM(NON-1) MARKER).
L -> M (IN GIM(NON-1) MARKER).
L -> M (IN GIM(NON-1) MARKER).
/FTIA-VAR_003888.
                                                                                                                                                                                                                                                                                                                                                                                                            Length 330;
    INTERCHAIN (WITH HEAVY CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                             36106 MW; 3770EE106C2FA33D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             Score 541; DB 1;
Pred. No. 3.9e-48;
4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 91.8%;
Matches 101; Conservative
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204
308
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330
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1112
1112
1144
1250
130
97
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    DISULFID
DISULFID
DISULFID
DISULFID
                                        CARBOHYD
MOD RES
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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MISCELLANEOUS: Disease protein WIS is lacking most of the V region and all of the CH1 region.

-!- MISCELLANEOUS: Disease protein ZUC lack most of the V region, all of the CH1 region, and part of the hinge compared with normal gamma-3 heavy chains.

-!- MISCELLANEOUS: Disease protein OWM may represent an allelic form or another gamma chain subclass.

-!- MISCELLANEOUS: The hinge region in gamma-3 chains is about four times as long as in other gamma chains and contains three identical listresidue segments preceded by a similar 17-residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005624; C:membrane fraction; NAS.
GO; GO:0005624; C:membrane fraction; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR00310; Ig-11ke.
InterPro; IPR003597; Ig-c1.
InterPro; IPR003506; Ig-MHC.
Pfam; PF00047; ig; 2.
SNART; SNO047; ig; 2.
PROSITE; PS50355; IG-MHC; 1.
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DOMAIN 12 73
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Gaps

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5; Indels

9

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61 PREEQPINSTYRVVSVLTVLAQDMLNGKEYKCKVSNXGLPSSIEKTISKAK 110

174 PREEGYNSTYRVUSVETVLAQDWINGKEFKCKVSNKALPAPIEKTISKAK 223

Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxiD=9606; [1]

21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
16-Gramma-3 chain C region (Heavy chain disease protein) (HDC)
1GHG3.

RESULT 4
10 403 HUMAN
10 603 HUMAN
10 10 21-JU
11 15-MA
115-MA
11

STANDARD;

GC3_HUMAN P01860;

1 APPVAGGPSVFLFPPKPETLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK

gamma

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stocknoim (1490/).

-!- MISCELLANBOUS: Ref.1 sequence has the D12 allotypic marker,

104-Thr, and the B14 marker, 185-Thr. Ref.3 has the D11 and B15

markers and Ref.5 the B15 marker.

-!- SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                        MEDLINE=70110015; PubMed=5461106;
Fruchter R.G., Jackson S.A., Mole L.B., Porter R.R.;
Sequence studies of the Fd section of the heavy chain of rabbit
immunoglobulin G.";
Biochem. J. 116:249-259(1970).
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 129-131 AND 155-322.
Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
(In) Killander J. (eds.);
Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
Stockholm (1967).
                                                                                    Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L., "Heavy chain genes of rabbit 1g0: isolation of a cDNA encoding heavy chain and identification of two genomic C gamma genes.", Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.3%; Score 433; DB 1; Length 323; 72.5%; Pred. No. 4.6e-37; ive 12; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T -> M (IN D11 MARKER).
T -> A (IN E15 MARKER).
N -> B (IN E15 MARKER).
Q -> B (IN REF. 2).
Q -> B (IN REF. 2).
N -> D (IN REF. 3 AND 4).
N -> D (IN REF. 5).
O -> B (IN REF. 5).
N -> D (IN REF. 5).
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IG-LIKE 2.
IG-LIKE 3.
                                            SEQUENCE OF 88-266 FROM N.A.
MEDLINE-83299917; PubMed=6193512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M16426; AAA31289.1; -.. PIR; A91749; GHRB. HSSP; PO1877; 1FCL. InterPro; IPR007110; Ig-like. InterPro; IPR003597; Ig cl. InterPro; IPR003597; Ig cl. InterPro; IPR003606; Ig_MHC. Pfam; PP00047; ig; 3. PROSITE; S806407; IG_LIKE; PROSITE; PS06355; IG_LIKE; 3. PROSITE; PS062590; IG_MHC; 1.
ochem. J. 151:337-349(1975).
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Matches 79; Conservative
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CON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. PubMed-6313520; MBDLINE-84630930; Prom Distriction K.E., Alexander C.B., Mage R.G.; Bernstein K.E., Alexander C.B., Mage R.G.; Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE=76135469; PubMed=1243651;
Pract D.M., Mole L.E.;
"Sequence studies on the constant region of the Fd sections of rabbit
immunoglobulin G of different allotype.";
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CHAIN DIMER;
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Oyctcolagus cuniculus (Rabbit).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PREEQFINSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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Pred. No. 7.7e-46;
7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .).
REMOVED POST-TRANSLATIONALLY
                                                                     PYRROLIDONE CARBOXYLIC ACID. N-LINKED (GLCNAC. ).
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B69CBC95705B2F46 CRC64;
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N-LINEAC....).
INTERCHAIN (WITH HEAVY CO INTERCHAIN (WITH HEAVY CO
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QV -> EB (IN ZUC).

P -> L (IN ORM).

F -> Y (IN ORM).

P -> Y (IN ORM).

P -> Y (IN ORM).

T -> A (IN ORM).

T -> A (IN ORM).

FTICL=VAR_003893.
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g gamma chain C region.
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/FIId=VAR 00389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 87.3%;
Matches 96; Conservative
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       134
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290
127
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126
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                                                                        10044433227
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GC RABIT
AC PO1870;
DT 21-JUL-198
DT 21-JUL-198
DT 10-OCT-200
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Mammalia; Butheria; Rodentia; Hystricognathi; Cavidae; Cavia
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les 79; Conser
                               NCBI_TaxID=10141;
                                                                                                    SEQUENCE OF 1-3.
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brueggemann M.;
"Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
"Evolution of the rat immunoglobulin-like domains.
-!- SIMILARITY: Contains 3 immunoglobulin-like domains.
PIR; PS0018; PS0018.
HSSP; P01842; 7FAB.
InterPro; IPR003597; Ig.-1ike.
InterPro; IPR003597; Ig.-1.
InterPro; IPR003597; Ig.-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1998 (Gulles pig)
16-JUL-1998 (Gulles pig)
16-JUL-1998 (Gulles pig)
17-JUL-1998 (Gulles pig)
18-JUL-1998 (Gul
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                                                                                                              CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IG-LIKE 1.
1G-LIKE 2.
IG-LIKE 3.
INTERCHAIN (WITH A LIGHT CHAIN)
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69.7%; Pred. No. 4.7e-37;
iive 20; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                            01-FEE-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
gamma-2B chain C region.
Rattus norvegicus (Rat)
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INTERCHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=89232738; PubMed=3149946;
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333 AA;
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nes 76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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P01862;
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P20761;
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GC2_CAVPO
TD GC2_CAVPO
AC PO186
DT 21-JU
DT 21-JU
DT 11-JU
DE 119-JU
DE 119-JU
DE 10-JU
DE 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Turner K.J., Cebra J.J.;
"Structure of heavy chain from strain 13 guinea pig
immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
and hinge region cyanogen bromide fragments.";
Biochemistry 10:9-17(1971).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 114-226.
MEDINE=7303072; Pubmed=4429665;
Tracey D.E., Cebra J.J.;
Prinesy D.E., Cebra J.J.;
Prinary structure of the CH2 homology region from guinea pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEAVY CHAIN).
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19 INTERCHAIN (WITH A HEAVY CHA
107 INTERCHAIN (WITH A HEAVY CHA
110 INTERCHAIN (WITH A HEAVY CHA
202
178 N-LINKED (GLCNAC. . .) .
308
1, 36074 MW; 5D231B7164D1FBA9 CRC64;
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                                                                                                                                                         SEQUENCE OF 4-68.

MEDLINE=7.058471, PubMed=5538606;

Birshtein B.K., Hussain O.Z., Cebra J.J.;

Structure of heavy chain from strain 13 guinea pig

"Structure of heavy chain from strain 13 guinea pig

"munuoglobulin-G(2) 3. Amino acid sequence of the rainf-constructure ioining heavy and light chains.";

Biochemistry 10:18-25(1971).
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Trischmann T.M.;
Submitted (APR-1975) to the PIR data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 69-133 AND 312-329.
MEDLINE=71058486; PubMed=5538616;
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MEDLINE=71058474; PubMed=4922544;
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                                                                                                                                                                                                                                                                   01-AUG.1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annocation update)
16 gamma-3 chain C region, secreted form.
Mus musculus (Mouse).
Eukaarjota (Aranie, Craniata, Vertebrata; Buteleostomi; Mamajia; Butheria; Rodentia; Sciurognathi; Muridae; Musinee; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 KPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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62 REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                   HSSP, PO1877, 1PC1.
InterPro; IRRO07110; Ig-like.
InterPro; IRRO03006; Ig_C1.
InterPro; IRRO03006; Ig_Met.
InterPro; IRRO03006; Ig_Met.
PRAM; PP00047; Ig; 3.
PROSITE; PS50836; IG_LIKE; 3.
PROSITE; PS003200; IG_Met.; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Irmunoglobulin Alternative splicing.
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01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g gamma-3 chain C region, membrane-bound form.
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PIR; B02156; G3MSC.
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98 113 HIN
114 223 CH2
224 327 CH3
329 AA; 36228 NW; F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Gaps
                                                                                                                                                                                                                  Wall R.; The structure of the mouse immunoglobulin in gamma 3 membrane gene
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R HSSP; PO1857; JSFCI.

R InterPro; IPR007110; ig-like.

R InterPro; IPR007110; ig-like.

R InterPro; IPR003597; ig_c1.

R PR0017; ig; 3.

R PROSITE; PS500835; IG_LIKE; 3.

R PROSITE; PS00290; IG_MHC, 1.

Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;

W Transmembrane; Alternative splicing.

NON TER 1 97 CH:

T DOWLIN 114 223 CH:

T DOWLIN 224 327 CH3.

T TRANSMEM 346 362 POTENTIAL;

T DOWLIN 224 327 CH3.

T TRANSMEM 346 362 POTENTIAL;
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MEDLINE=85027161; PubMed=6092053;
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine 1gG3 constant region gene.";
EMBO J. 3:2041-2046(1984).
                                                                                                                                                                   SEQUENCE OF 328-398 FROM N.A.
MEDLINE=84041483; PubMed=6314258;
Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
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E -> Q (IN REF. 2).
P -> F (IN REP. 2).
CP7F264B50A41B95 CRC64;
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HINGE.
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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(Rel. 01, Last sequence update)
(Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                        Nucleic Acids Res. 11:6775-6785(1983)
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J00451; AAB59655.1; -.
EMBL; V01526; CAA24767.1; ALT_SEQ.
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398 AA;
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15-MAR-2004 (
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P01868;
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus

(Mouse)

NCBI_TaxID=10090;

SEQUENCE OF 70-322 FROM N.A. (MYELONA PROTEIN MOPC 21).
MEDLINE=80012837, PubMed=113776;
KOGERS J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTBIN MOPC 31C).
MEDLINE=80202559; PubMed=6769752;
Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
cloned in a bacterial plasmid.";
Gene 9:87-97(1980). SEQUENCE FROM N.A.

MEDLINES BRO04505; PubMed=115593;

Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,

Takahashi N., Mano Y.;

"Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";

Cell 18:559-568 [1979]. Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Muxinae, Mus Svasti J., Milstein C.;
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Biochem. J. 126:837-850(1972).
-!- SUBCELLULAR LOCATION: Secreted.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2; "Evolution of immunoglobulin subclasses. Primary structure of Isold=P01868-1; Sequence=Displayed;
Note=May be the major isoform;
Name=Membrane-bound; IsoId=P01869-1; Sequence=External; gamma-1 chain C region secreted form. heavy chain."; Nucleic Acids Res. 6:3305-3321(1979) SEQUENCE (MYELOMA PROTEIN MOPC 21). MEDLINE=78242288; PubMed=98524; murine myeloma gammal chain."; J. Biol. Chem. 253:6068-6075(1978). MEDLINE=73008889; PubMed=5073237; MGD; MGI:96446; Igh-4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 2.
PMART; SM04077; IGc1.
PROSITE; PS00290; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1. [5] DISULFIDE BONDS (MOPC 21) musculus (Mouse) Name=Secreted; Mammalia, Eutheri NCBI_TaxID=10090; Adetugbo K.;

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EMBL; V00793; CAA24172.1; -...
EMBL; V00793; CAA24173.1; -...
EMBL; V00793; CAA24174.1; -...
EMBL; V00793; CAA24175.1; -...
EMBL; V00795; CAA24175.1; -...
EMBL; A02159; GAA24176.1; -...
PIR; A02159; GIMS.

Immunoglobulin C region; Glycoprotein; CH1. HINGE. CH2. CH3.	INTERCHAIN (WITH A LIGHT CHAIN). INTERCHAIN (WITH A HEAVY CHAIN). INTERCHAIN (WITH A HEAVY CHAIN). INTERCHAIN (WITH A HEAVY CHAIN). N-LINKED (GLCNAC).	REMOVED POST-TRANSLATIONALLY. N -> D (IN REF. 3). N -> D (IN REF. 3). W, A338812F3D1F2C93 CRC64; Score 405; DB 1; Length 324; Pred. No. 3.4e-34; 18; Mismatches 13; Indels 0; Gaps 0;	SVTLEPPREKOTLMISRTPEVICVVUDVSQEDFEVQFNWYVDGVEVHNAKTKPREEQFNS 68 [:
in; Immu ig. 1 97 110 217 224	1002 11004 1109 1109	324 276 278 35704 MW; 69.5%; 69.5%; ative 18	OTLMISE: OVLTITL' THODWING::
ulin domai e splicing 1 1 98 1 111 2 218 3	1001 1001 1009 1009 148	ო -ქ	VFLEPPKPI : VFIFPPKPI XRVVSVLT' : FRSVSELP:
Immunoglobulin domain; Alternative splicing. NON TER 1 1 1 DOMAIN 1 97 DOMAIN 98 110 DOMAIN 218 324 DOMAIN 218 324	DISULTID DISULTID DISULTID DISULTID DISULTID CARBOHYD	MOD RES CONFLICT CONFLICT SEQUENCE Query Match Best Local Sim	0 11 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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Eukaryota; Meirzoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090; Honjo T., Obsta M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T., Takahashi N., Mano Y.; **Cloning and complete nucleotide sequence of mouse immunoglobulin SEQUENCE OF 323-393 FROM N.A.
MEDLINE-82197626; PubMed-6804950;
MFDLINE-82197626; PubMed-6804950;
YJOER S.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
"mRNA for surface imminoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular GCIM_MOUSE STANDARD; PRT; 393 AA.
P01865;
10.1011-1996 (Rel. 01, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
10.0CT-2003 (Rel. 42, Last annotation update)
10.3 gamma-1 chain C region, membrane-bound form.
Mus musculus (Mouse) SEQUENCE FROM N.A. MEDLINE=80045036; PubMed=115593; gamma 1 chain gene."; Cell 18:559-568(1979) domain."

MEDLINE-82115295; PubMed-6792207; Rogers J., Choi B., Souza L., Carter C., Word C.J., Kuehl M., Bisenberg D., Wall R.; Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains."; Cell 26:19-27 Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982). SEQUENCE OF 323-366 FROM N.A.

SEQUENCE OF 1-44 FROM N.A. MEDLINE=82222190; Pubmed=6283537;

329 AA

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                                                                                                    Rāttus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINB=88166903; PubMed=3127222;
MEDLINB=88166903; PubMed=3127222;
MEDLINB=88166903; PubMed=3127222;
Sequence of a rat immunoglobulin gamma 2c heavy chain constant region cDNA: extensive homology to mouse gamma 3.";
Eur. J. Immunol. 18:317-319(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP, P01842, 7FAB.

InterPro; IPR007110, Ig-like.

InterPro; IPR0031096; Ig_MHC.

Pfam; PF00047; ig; 2.

SMART; SW00407; IGC1: 2.

PROSITE; PS00836; IG_LIKE; 3.

PROSITE; PS00830; IG_MHC, 1.

Immunoglobulin domain; Immunoglobulin C region.
                                        01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
115-UUL-1999 (Rel. 38, Last annotation update)
19 gamma-2C chain C region.
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                 STANDARD;
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Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
"Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
                                                                                                                                                                                                                                                                                                                                    R PIR; B02159; GJMSM.

R PIR; B02159; GJMSM.

R PDB; 15C9; 23 "AR-99.

R PDB; 1CL7; 12-JAN-00.

R PDB; 1T1; 06-FRB-01.

R PDB; 1T1; 06-FRB-01.

R PDB; 1KC5; 24-JUL-99.

R PDB; 1KC5; 24-JUL-99.

R PDB; 1KC7; 11-AX-02.

R PDB; 1KC8; 10-JUL-99.

R MGD; MGI 16-GLF.

R MGD; MGI 16-GLF.

R MGD; MGI 16-GLF.

R MGD; 1GC 1.

R INTERPORT 10-JUL-99.

R PROSITE; PSC0805; IG MHC.

T DOWAIN 98 110 HINGE.

T DOWAIN 111 217 CH2.

T POWAIN 111 217 CH2.
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69.6%; Pred. No. 4.3e-34;
iive 18; Mismatches 13; Indels
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CYTOPLASMIC (POTENTIAL).
4CC88343B7A1CE27 CRC64;
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                                                                        Event=Alternative splicing; Named isoforms=2; Name=Membrane-bound;
                                                                                                         IsoId=P01869-1; Sequence=Displayed;
                                                                                                                  Name-Secreted;
IsoId=P01868-1; Sequence=External;
Note=May be the major isoform;
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393 AA;
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                                                                                                                                                                                       6 GGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPBVQFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                     0; Gaps
INTERCHAIN (WITH A HEAVY CHAIN) INTERCHAIN (WITH A HEAVY CHAIN)
                                                                                                             69.1%; Score 403; DB 1; Length 329; 68.6%; Pred. No. 5.6e-34; ive 17; Mismatches 16; Indels
                                                                                                                                                                                                                                                                   66 FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                     36571 MW; SFCD7B7933850773 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
11g gamma-2B chain C region secreted form.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 336 AA
                                                                                                                                     Local Similarity 68.6
nes 72; Conservative
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P01866;
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GCB MOUSE
ID GCB M
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DT 21-JU
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Local Similarity 69.69

Best Loc Matches

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TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110

176

RESULT 12

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0; Gaps

INTERCHAIN (WITH A LIGHT CHAIN)

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Isold=Boll&66-1; Sequence=Displayed;
Note=May be the major isoform;
Note=May be the major isoform;
Isold=Boll&6-1; Sequence=External;
Isold=Boll&6-1; Sequence=External;
-!- FTM: 0-LINKED GLYCAN CONSISTS OF GAL-GALMAC DISACCHARIDE WHICH IS MODIFIED WITH 2 SIALIC ACID RESIDUES.
-!- PTM: DISCRILANEOUS; The a lalele sequence is shown.
-!- MISCELLANEOUS; The a lalele sequence is shown.
-!- SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ALLELE B).
MEDLINE-82173203; PubMed-6803173;
Ollo R., Rougeon F.;
"Mouse immunoglobulin allotypes: post-duplication divergence of gamma 2s and gamma 2b chain genes.";
Nature 296:761-763(1982).
                                                                                                                                            Tucker P.W., Marcu K.B., Slightom J.L., Blattner F.R.;
"Structure of the constant and 3' untranslated regions of the murine gamma 2b heavy chain messenger RNA.";
Science 206:1299-1303(129).
                                           SEQUENCE FROM N.A. (ALLELE A).
MEDLINE-80120716; PubMed-e766534;
Yamawaki-Kataoka Y., Kataoka T., Takahashi N., Obata M., Honjo T.;
"Complete nucleotide sequence of immunoglobulin gamma2b chain gene
cloned from newborn nouse DNA.";
Nature 283:786-789(1980).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rođentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                              MEDINB=80081502; PubMed=117549;
Tucker F.W., Marcu K.B., Newell N., Richards J., Blattner F.R.;
"Sequence of the cloned gene for the constant region of murine g
2b immunoglobulin heavy chain.",
                                                                                                                                                                                                                                                                                                                                                          CARBOHYDRATE-LINKAGE SITZ THR-105.
MEDLINE-94216359; PubMed=7512967;
Kim H., Yamaguchi Y., Masuda K., Matsunaga C., Yamamoto K.,
Irimuxa T., Takahashi N., Kato K., Arata Y.;
FO-glycosylation in hinge region of mouse immunoglobulin G2b.F;
J. Baol Chem. 269:12245-12350(1994).
--- SUBCELLULAR LOCATION: Secreted (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN).
CHAIN).
CHAIN).
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HSSP; PO1042; 7PAB.
InterPro; IPR00110; 1g-like.
InterPro; IPR00110; 1g-like.
InterPro; IPR003597; 1g-c1.
InterPro; IPR003006; 1g_MHC.
Pfam; PR00047; ig; 3.
PROSTIE; PS50835; IG LiKE; 3.
PROSTIE; PS00290; IG_MHC; 1 Immunoglobulin C region; Glycoprotein; Alternative splicing; Repeat.
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IG-LIKE 2.
INTERCHAIN (WITH A LIGHT CHAIN)
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INTERCHAIN
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                                                                                                                        SEQUENCE FROM N.A. (MPC 11).
MEDLINE=80081501; PubMed=117548;
                                                                                                                                                                                                                                                           Science 206:1303-1306(1979).
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2226
331
15
109
112
112
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210
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                     NCBI_TaxID=10090;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                       (GALNAC. . . ) .
POST-TRANSLATIONALLY (PROBABLE) .
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Isold=P01866-1; Sequence=External;
Note=May be the major isoform;
-!- PTM: DISULFIDE BONDS BY HOWOLOGY WITH OTHER IG GAMMA CHAINS.
-!- PTM: DISULFIDE BONDS BY HOWOLOGY WITH OTHER IG GAMMA CHAINS.
-!- MISCELLANBOUS: The sequence of residues 1-335 is assumed to be identical with the corresponding region of the secreted form.
-!- MISCELLANBOUS: The a allels sequence is shown.
-!- SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 335-405 FROM N.A.
MEDLINE=82222190; PubMed=6283537;
Yamawaki: Kataoka Y., Nakai S., Miyata T., Honjo T.;
Yamawaki: Kataoka Y., Nakai S., Miyata T., Honjo T.;
Mucleotide sequences of gene segments encoding membrane domains immunoglobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PREBQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 THREDYNSTIRVVSTLPIQHQDWASGKEFKCKVNNKDLPSPIERTISKIK
                                                                                                                                                                                                                                                                                         Match 68.4%; Score 399; DB 1; Length 336; Local Similarity 65.5%; Pred. No. 1.5e-33; les 72; Conservative 18; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Souza L., Carter C., Word C.J., Kuehl
                                                               Q -- N (IN ALLELE B).
T -- A (IN ALLELE B).
N -- D (IN ALLELE B).
M -- I (IN ALLELE B).
I -- S (IN REF. 2 AND 3).
I -- T (IN REF. 2 AND 3).
I -- T (IN REF. 2 AND 3).
I -- T (IN REF. 2 AND 3).
M; 7D879662607C356E CRC64;
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Rogers J., Choi E., Souza L., Carter C., Word C.J., Kue Risenberg D., Wall R.;
"Gene segments encoding transmembrane carboxyl termini immunoglobulin gamma chains.";
Cell 26:19-27(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bvent=Alternative splicing, Named isoforms=2,
Name=Membrane-bound;
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21-717.
01-AUG-1991 (Rel. 19, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
19 gamma-2B chain C region, membrane-bound form.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=P01867-1; Sequence=Displayed;
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  336 AA;
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DISULFID
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GCBM MOUSE
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us-09-674-857-12.rsp

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Gaps
11-Jul. 1986 (Rel. 01, Created)
21-Jul. 1986 (Rel. 01, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
16 gamma-2A chain C region secreted form (B allele).
18 July musculus (Mouse).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=82037777; PubMed=6794027;

MEDLINE=82037777; PubMed=6794027;

Dognin M.J., Lauwereys M., Strosberg A.D.;

Milliple amino acid substitutions between murine gamma 2a heavy chain For regions of Igla and Iglb allotypic forms.";

Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).

-! SUBCELLULAR LOCATION: Secreted (Potential).

-! ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Name=Secreted;
                                                                                                                                                                                                                                                                                                                    .
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                                                                                                                                                                                            CHAIN).
CHAIN).
CHAIN).
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STRAIN=CSPBL/6;
MEDLINE=82037861, PubMed=6170065;
Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D
"Multiple differences between the nucleic acid sequences of "
"Iggzaa and IgGzab alleles of the mouse.";
Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
                                                                                                                                              IG-LIKE 1.
1G-LIKE 2.
IG-LIKE 3.
INTERCHAIN (WITH A LIGHT CHAIN)
                                                                                                                                                                                                                                                                                               / Match
Local Similarity 65.5%; Pred. No. 1.8e-33;
ies 72; Conservative 18; Mismatches 20; Indels
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CYTOPLASMIC (POTENTIAL).
89B3CF0A9B6D49FA CRC64;
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GCAB_MOUSE
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Search completed: April 29, 2004, 08:44:54 Job time : 11 secs

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R PDB; 180G; 23-MAR-99.

R PDB; 1HH6; 26-JAN-01.

R PDB; 1HH6; 24-JUL-03.

R PROVITS; PS00290; IG_MHC.

R RACH; 13-2.

R PROSITE; PS00290; IG_MHC; 1.

M Immunoglobulin domain; Immunoglobulin C region; Alternative splicing; J POMÄIN 6 98 IG_LIKE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 APPVAGGPSVFLFPPKPKDTIMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                 Isoid=P01865-1; Sequence=External;
-!-MISCIADROYS: The sequence differs from that of the a allele,
from BALB/C mice, at 15% of the positions.
-!- SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PREBOFNSTYRVVSVLTVLHODWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 THREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNRALPSPIEKTISKPR
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llarity 64.5%; Pred. No. 3e-33;
Conservative 19; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=P01864-1; Sequence=Displayed;
Note=Probably the major isoform;
Name=Membrane-bound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 71; Conserval
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Matches
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April 29, 2004, 08:41:02; Search time 36 Seconds (without alignments) 964.083 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM protein - protein search, using sw model Run on:

US-09-674-857-12 583 1 APPVAGGPSVFLFPPKPKDT......CKVSNKGLPSSIEKTISKAK 110 BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Scoring table: Sequence:

1017041 segs, 315518202 residues Searched: 1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL 25:* Database :

sp_archea:*
sp_baceria:*
sp_baceria:*
sp_human:*
sp_human:*
sp_nammal:*
sp_organelle:*
sp_organelle:*
sp_phage:*
sp_plant:*
sp_virus:*
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sp_virus:* sp_archeap:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMAKIES	ţ	1	QBTC63	Q7Z7P5	Q725W1	Q7Z351	Q96PQ8	OBNF17	Q8N4Y9	Q86TT2	Q95M34	Q7TMK1	Q8R3V9	Q9R1A4	Q99LC4	091205	Q8R3H6	Q9D8L4
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		Score	565	541	541	541	543	534	534	531	462	417	409	405	405	399	399	396
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468 11 Q99L31 473 11 Q99L25 375 4 Q86TT1 598 4 Q9WUX4 597 4 Q9WUX4	'चचचच	618 4 Q96AA6 234 4 Q72473 236 4 Q723X4 239 4 Q8NEKO 239 4 Q8TCDO 613 11 Q8VCX7	90 900	493 4 QBNCL6 494 4 Q96K68 496 4 Q96DK0 496 4 Q96KX8 499 4 QBN5K4 684 13 Q90544
384 65.9 384 65.9 138 23.7 138 23.7		138 23.7 133 22.8 133 22.8 133 22.8	វល់ដល់លល់ស	120.5 20.7 120.5 20.7 120.5 20.7 120.5 20.7 120.5 20.7 118.5 20.3
17 18 19 20 21	122222 12224 12548	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		ቀ ቁ ቁ ቁ ቁ ቁ ቁ ዕ ዛ ሪ ሠ ሴ ሲ

ALIGNMENTS

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0; Gaps
                                                    QBTG63;
QBTG63;
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Eukaryota, Metazoa; Conordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Butheria, Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                            P III

C TISSUE=Kidney;

A Strausberg R.;

Strausberg R.;

Submitted (MAR-2002) to the EMEL/GenBank/DDBJ databases.

EMBL; BC025985; AAH25985.1; -.

EMBL; BC025989; AAH25985.1; -.

GO; GO:0005507; F:copper ion binding; IEA.

GO; GO:0005489; F:electron transporter activity; IEA.

GO; GO:0006189; F:electron transporter activity; IEA.

GO; GO:0006181; F:electron transporter activity; IEA.

InterPro; IPR0019023; BlueCu_1.

R InterPro; IPR001906; Ig_MHC.

InterPro; IPR003596; Ig_WHC.

InterPro; IPR003596; Ig_WHC.

R PROSTITS; PS00196; COPPER_BLUE; 1.

R PROSTITS; PS00196; COPPER_BLUE; 1.

R PROSTITS; PS00290; IG_MHC; 3.

H Hypothactical protein.

Q SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

96.9%; Score 565; DB 4; Length 473;
Best Local Similarity 97.3%; Pred. No. 2e-55;
Matches 107; Conservative 0; Mismatches 3; Indels
                                    PRT; 473 AA
                                    PRELIMINARY;
                                    QBTC63
RESULT 1
Q8TC63
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1 APEVAGGESVELPPPKPKDTLMISRIPEVICVVDVSQEDPEVQFNWYVDGVEVHNAKIK 60

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RESULT 4
Q7Z351
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A RISUBENDIEGE;

A RIBDLINE=22388257; PubMed=12477932;

A RIABSER R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

B Aptichento M., Soares M.B., Bornaldo M.F., Casavant T.L., Scheefer T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B Robar S.A., McEwan P.J., McKernan K.J., Abrameon R.D., Mullahy S.J.,

B Soak S.A., McEwan P.J., McKernan K.J., Abrameon R.D., Mullahy S.J.,

B Nillalon D.K., Muzny D.M., Sodergra R.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

B Niting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Nodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Chomes S.J., Marran M.A.,

Chones S.J., Marran M.B.,

Chones S.J., Marran M.B.,

Chones S.J., Marran M.B.,

Chones S.J., Chones S.J.,

Chones S.J., Marran M.B.,

Chones S.J., Chon
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257 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 APPVAGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                       PREBQPNSTYRVUSULTVLHQDMLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PREEDFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PREEQYNSTYRVVSVLTVLAQDWLNGKEYKCKVSNKALPAPIEKTISKAK 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 91.8%; Pred. No. 1e-52;
Matches 101; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Strausberg R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC051328; AAH51328.1; -.
Hypothetical protein.
SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;
                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                        01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, Hypochetical protein. Homo sapiens (Human).
                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Spleen;
                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
Q7Z5W1
ID Q7Z5
AC Q7Z5
AC Q7Z5
DT 01-0
DT 01-0
DT Hypo
                                                                                                                                              RESULT 2
Q7Z7PS
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Last sequence update) Last annotation update)

Created)

(TrEMBLrel. 25, (TrEMBLrel. 25, I

01-OCT-2003 (TrEMBLrel 01-OCT-2003 (TrEMBLrel 01-OCT-2003 (TrEMBLrel Hypothetical protein.

PRT;

PRELIMINARY;

Q7Z5W1 Q7Z5W1;

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MEDINE-20188257; PubMed=12477932;

MEDINE-20188257; Medin E.S., Medere E.C.F., Bhat N.K.,

MEDINE-20188257; Medin E.S., Moore T., Max S.L., Wang J., Haich F.,

MEDINE-20188257; Medin E.S., Moore T., Max S.L., Wang J., Haich F.,

MEDINE-20188257; Medin E.S., Moore T., May S.L., Mang J., Haich F.,

MEDINE-20188258, Modern E.S., Medin M.S., Malek J.A., Gunarathe F.H.,

Medinary S.S., Modern P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Medinary S.S., Muzny D.M., Sodergen E.J., Lu X., Gibbs R.A.,

Milaton D.K., Muzny D.M., Sodergen E.J., Lu X., Gibbs R.A.,

Milaton D.K., Muzny D.M., Sodergen E.J., Lu X., Gibbs R.A.,

Milaton M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Milaton W.M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Milaton W.M., Staiska U., Schmutz J., Myers R.M., Butterfield Y.S.,

A zzywinski M.I., Skaiska U., Smailus D.E., Schnerch A., Schein J.E.,

Mediguez A.C., Grimwood J., Smailus D.E., Schnerch A., Schein J.E.,

Mediguez A.C., Marza M.A.;

Medical analysis of more than 15,000 full-length human mouse CDNA sequences."

Medical mouse CDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 APELLGGPSVFLPPPKXDTLMISRTPBVTCVVVDVSHBDPEVKFNWYVDGVEVHNAKTK 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 APPVAGGESVFLPPKEKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
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TISSUB-Human rectum tumor;
Blocker H., Boccher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Fobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
Hypothetical protein.
SEQUENCE 482 AA; 52852 MW, EDA75F1901D1A034 CRC64;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NGBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PREEQFINSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Straugherg R.;
Straugherg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC05384; AAH53984.1; -.
Hypothetical protein.
SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     072351 PRELIMINARY; PRT; 482 AA.
01-037-2503 (TERMBirel. 25, Created)
01-0CT-2003 (TERMBirel. 25, Last sequence update)
01-0CT-2003 (TERMBirel. 25, Last annotation update)
Hyporhetical protein DKPZp686N02209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Juences.";
Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Spleen;
                                                                                                                                                                     FROM N.A.
                                                                                                                                                                     SEQUENCE
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us-09-674-857-12.rspt

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                                                                                     266 APELLGGBSVFLPPPKPKDTLMISRTPBVTCVVVDVSHEDPBVXFNWYVDGVBVHNAKTK 325
                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=21477448; PubMed=11593034;
Hu Z., Garen A.,
"Targeting tissue factor on tumor vascular endothelia! cells and tumor cells for immunotherapy in mouse models of prostatic cancer.";
Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
                                                                  1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
                                 Gaps
                                                                                                                                                                                                                                                                     096PQ8;
01-DBC-2001 (TrEMBLrel. 19, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Factor VII active site mutant immunoconjugate.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                ;
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IN 2., Garen A.;

Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

R GNBL; AF27774; AAK5866.2;

R GO; GO:0005576; C:extracellular; IEA.

GO; GO:0004256; F:calcium ion binding; IEA.

GO; GO:0004256; F:trypsin activity; IEA.

InterPro; IPR000132; Asx hydroxyia.

R interPro; IPR00132; Asx hydroxyia.

R interPro; IPR00138; EGF_I.

R interPro; IPR00138; 
   Length 482;
                                 5; Indels
92.8%; Score 541; DB 4;
91.8%; Pred. No. 1.1e-52;
tive 4; Mismatches 5;
                                                                                                                                                                                                                                                      619
                   Best Local Similarity 91.8
Matches 101; Conservative
                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
   Query Match
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                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUB-Spleen;
Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
"The nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                                                                                                                                                                                                  61 PREEQFWSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 PREEQFNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expansion of the EMBL/GenBank/DDBJ databases.

REMBL; AK090464; BAC03445.1; -...

REMBL; AA5094, A45874.

R InterPro; IPR00110; Ig-11ke.

R InterPro; IPR003597; Ig_c1.

R InterPro; IPR003506; Ig_MHC.

R Pfam; PF00047; Ig. 3.

R Pfam; PF00047; IG. 1; 3.

R PROSITE; PS00835; IG_MHC; 2.

NON_TER
                                                                                                                                          Length 679;
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91.6%; Score 534; DB 4; Length 50
Best Local Similarity 90.9%; Pred. No. 7.1e-52;
Matches 100; Conservative 3; Mismatches 7; Indels
                                                                                                                                          92.8%; Score 541; DB 4; Length 67 91.8%; Pred. No. 1.6e-52; cive 4; Mismatches 5; Indels
PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN ER; 1.
SEQUENCE 679 AA; 75552 WW; 0B0023AE70A067A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 509 AA; 56111 MW; 089498D8076E863C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
PLJ00385 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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                                                                                                                                            Query Match
Best Local Similarity 91.8<sup>†</sup>
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             spleen.";
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Q8N4Y9;
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
QBNF17
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us-09-674-857-12.rspt

Length 354;

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01-JUN-2003 (TERMBLE). 24, Last sequence update)
01-JUN-2003 (TERMBLE). 24, Last sequence update)
01-JUN-2003 (TERMBLE). 25, Last sequence update)
Human full-length cDNA clone CS0D1019YP20 of placenta of Homo sapiens
(Human) (Fragment).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                         TISSUENCE FROM N.A.

TISSUEDE-Primary B-Cells;
Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

REMBL; BC033178; AAH33178:1; -.
RITERPRO; IPR00110; Ig-like.
RITERPRO; IPR003597; Ig-ci.
RITERPRO; IPR003597; Ig-ci.
RITERPRO; IPR003597; Ig-ci.
RITERPRO; IPR003596; Ig-v.
R Pfam; PF00047; ig; 4.
SWART; SW004067; IG-V.
R SWART; SW004067; IG-V.
R PROSITE; PS50835; IG-LIKE; 4.
R PROSITE; PS50835; IG-LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGUENCE FROM N.A.

TISSUE=Placenta;

Li N.B., Garuber C., Jessee J., Polayes D.;

Li N.B., Garuber C., Jessee J., Polayes D.;

Li N.B., Garuber C., Jessee J., Polayes D.;

Li Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

EMBL: BX248278; CAD62606.1;

R GO; GO:046821; C.extrachromcsomal DNA; IEA.

R GO; GO:046821; C.extrachromcsomal DNA; IEA.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR00306; Ig-MHC.

R Pfam; PF00047; Ig-1;

R PROSITE; SM0047; IG-1;

R PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.6%; Score 534; DB 4; Length 52 ilarity 90.9%; Pred. No. 7.3e-52; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoscope;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 521 AA; 57156 MW; ZAC7D22E72D6CAA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354 AA; 39125 MW; 23B80BF4D2B87A92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 100; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-Placenta;
                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON TER
SEQÜENCE
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MEDINE=98383415; PubMed=9717671;
MEDINE=98383416; PubMed=9717671;
Magner B., OvereeOn G., Sheoran A., Holmes M., Richards C.,
Magner B., OvereeOn G., Sheoran A., Holmes M., Richards C.,
Leibold W., Radbruch A.;
Teibold W., Radbruch A.;
"Organization of the equine immunoglobulin heavy chain constant region genes. II. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
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III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
III. Alignment of c-mu, c-gamma, c-
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                                                                                                           1 APPVAGGPSVFLFPPKPKDTLMISRTPBVTCVVVDVSQBDPEVQFNWYVDGVBVHNAKTK
                                                          Gaps
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Buks musculus (Woolse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laura...
Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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                                                                                                                                                                                                              61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DCT-2003 (TrEMBLrel. 25, Last annotation update)
Immunogobulin gamma 1 heavy chain constant region (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.2%; Score 462; DB 6; Length 33 llarity 74.5%; Pred. No. 6.3e-44; Conservative 16; Mismatches 12; Indels
Query Match 91.1%; Score 531; DB 4; Length 35 Best Local Similarity 90.0%; Pred. No. 9.9e-52; Matches 99; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wagner B.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 470 AA
                                                                                                                                                                                                                                                                                                                                                                                                                 337 AA
                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1] -
SEQUENCE PROM N.A.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                 Q95M34
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                                                                                                                                                                                                                                                                                                                                                                                          295M34
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68

Gaps

Length 469

al protein. 469 AA; 51976 MW; 534793F155D05457 CRC64;

SO WERE THE REPRESENTATION OF THE PROPERTY OF

437 437 AA; 437 NON TER NON TER SEQUENCE 253 PPGNILGGESVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVFVSWFVDNKEVHTAWT 312 2 PP--VAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKT 59 Gaps 2; Length 470; Query Match 71.5%; Score 417; DB 11; Length 4' Best Local Similarity 67.6%; Pred. No. 1.2e-38; Matches 75; Conservative 17; Mismatches 17; Indels Last sequence update) Last annotation update) Created)

Mus musculus (Mouse). Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NOBI_TaxiD=10090; Strauberg R.;
MGD;
MG15446; Igh-4.
Interpro; IPR00110; Ig-like.
Interpro; IPR003306; Ig-WHC.
Interpro; IPR003306; Ig-WHC.
Interpro; IPR003596; Ig-W.
STRART; SM00406; IG-N;
SMART; SM00406; IG-LikE; 4. 01-JUN-2002 (TEMBLEEL 21, 01-JUN-2002 (TEMBLEEL 21, 01-OCT-2003 (TEMBLEEL 25, Hyporhetical protein. PRELIMINARY; SEQUENCE FROM N.A. **QBR3V9** RESULT 11
008R3V9
AC 08R3V
AC 08R3V
DT 01-JV
DT

(TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)

463 AA

PRT;

PRELIMINARY;

Q99LC4

DT 000

RESULT 13

099LC4; 01-JUN-2001 (

ö 288 261 SVPIFPPKFKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTKPREEQFNS 320 68 monoclonal 9 SVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREBQFNS Programmer FRCM N.A.

A wilde K.G., Yu.X., Exramoddoullah A.K.M., Misra S.;

Wilde K.G., Yu.X., Exramoddoullah A.K.M., Misra S.;

Wilde K.G., Yu.X., Exramoddoullah A.K.M., Misra S.;

T cloning of consa encoding for anti-white pine blister rust monoclona antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (ScFV).";

Embl. AP152372, AAD40243.1;

EMBL, AP152372, AAD40243.1;

PR PDB; 1CQK; 11-SEP-99.

R PDB; 1CQK; 11-SEP-99.

R PDB; 1CQK; 11-SEP-99.

R PDB; 1CQK; 11-SEP-97.

R PRO37775; SSO0335; 1G_LIKE; 4.

R PROS7775; PSSO0335; 1G_LIKE; 4. Gaps Mus musculus (Mouse). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus. Musl. MCBI_TaxID=10090; ö Query Match
69.5%; Score 405; DB 11; Length 437;
Best Local Similarity 69.6%; Pred. No. 2.5e-37;
Matches 71; Conservative 18; Mismatches 13; Indels 69 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110 289 TFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTK 330 69 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110 48142 MW; 5C3A7BB3EE7D697C CRC64; 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Garmal heavy chain of Mab7 (Fragment). 437 AA PRELIMINARY; Q9R1A4 Q9R1A4; IGH-4. g q ે ò

Matches

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Search completed: April 29, 2004, 08:46:18 Job time : 36 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 SVPLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNS 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C91205;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
AU044919.
Nan musculus (Mouse).
Eukaryota, Metazoa; Chordaca; Craniata; Vertebrata; Euteleostomi; Mazmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 11 LaxID=10090;
                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus
MCBI_TaxIb=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 463;
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Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitteed (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010327; ABH10327.1;
MGD; MGI:21449567; AM044919.
GG; GG:0005489; F:electron transporter activity; IEA.
GG; GG:0005489; F:electron transport; IEA.
GG; GG:0005418; F:electron transport; IEA.
InterPro: IPR007110; IG-1\overline{IEA}.
InterPro: IPR007110; IG-1\overline{IEA}.
InterPro: IPR003596; Ig_W.
FEAM; SMO&40; IG_W.
SMART; SMO&406; IGY; 1.
PROSITE; PS00190; CYTOCHROME_C; 1.
PROSITE; PS00190; IG_MHC; 1.
                                                                                                                                                                                                                              Strausberg R.;
Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC00343; AAH03435.1; -.
FIR, B45837; B45837.
HSSP; P01842; 7FBB.
MGD; MG1-96446; 1gh-R.
InterPro: IPR00110; 1g-1ike.
InterPro: IPR0013596; 1g_V.
Fran; PF00047; 1g; 3.
SNART; SM00406; 1Gy. 1.
PROSITE; PS0035; 1G_LIKE; 4.
PROSITE; PS00395; 1G_LIKE; 4.
PROSITE; PS00395; 1G_LIKE; 4.
SROGENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
69.5%; Score 405; DB 11; Length 4
Best Local Similarity 69.6%; Pred. No. 2.7e-37;
Matches 71; Conservative 18; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  il protein.
473 AA; 51946 MW; CF625F008932AF12 CRC64;
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to RIKEN cDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   473 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                           SEQUENCE FROM N.A.
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SEQUENCE 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PREEQFNSTYRVVSVLTVLHODMLNGKEYKCKVSNKGLPSSIEKTISKAK 110 | ... | | ... | | ... | | ... | | ... | | ... | | ... | | ... | | ... | | ... | | ... | | ... | | ... | | ... | | ... | | ... | | ... | | ... | | ... | | ... | | ... | | ... | | ... | | ... | | ... | | ... | | ... | ... | ... | 367
                                                                                                       y Match 68.4%; Score 399; DB 11; Length 474; Local Similarity 65.5%; Pred. No. 1.3e-36; hes 72; Conservative 18; Mismatches 20; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; BC025447; AAH55447.1; -.

R MGD; MGI:2144967; AU044919.

R GO; GO:0005489; F:electron transporter activity; IEA.

GO; GO:0005489; F:electron transport. IEA.

InterPro; IPR000345; CytC_heme_BS.

R InterPro; IPR00045; CytC_heme_BS.

R InterPro; IPR00110; IG-11ke.

R InterPro; IPR00110; IG-11ke.

R InterPro; IPR00596; Ig_WHC.

R SWART; SMO0406; IGV; 1.

R PROSITE; PS00190; CYTOCHROME_C; 1.

R PROSITE; PS00190; CYTOCHROME_C; 1.

R PROSITE; PS00190; CYTOCHROME_C; 1.

R PROSITE; PS00190; IG_MHC; 1.

R PROSITE; PS00190; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                 QBR3H6
                                                                                                                                                                                                                                               RESULT 15
QBR3H6
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GenCore version 5,1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

April 29, 2004, 08:46:23 ; Search time 38.5 Seconds [without alignments] 791.970 Million cell updates/sec Run on:

US-09-674-857-12 583 Title: Perfect score:

1 APPVAGGPSVFLPPPKPKDT......CKVSNKGLPSSIEKTISKAK 110 Seguence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

Total number of hits satisfying chosen parameters:

1138120 seqs, 277189581 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match: 08 Maximum Match: 1008 Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgr2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgr2_6/ptodata/2/pubpaa/PCT_MPW PUBL_Pep:*

3: /cgr2_6/ptodata/2/pubpaa/SCG_NEW PUBL_Pep:*

4: /cgr2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

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9: /cgr2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

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11: /cgr2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

11: /cgr2_6/ptodata/2/pubpaa/US09_NEW PUB.pep:*

13: /cgr2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

14: /cgr2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

15: /cgr2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

16: /cgr2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

17: /cgr2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

18: /cgr2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

19: /cgr2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

19: /cgr2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

10: /cgr2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

10: /cgr2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

10: /cgr2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ф					
Result	,	Query	:		!		
. OZ	Score	Match	Match Length DB	E C	ID	Description	
1	570	97.8	437	10	US-09-932-812-20	Sequence 20,	Apr
7	570	97.8	449	10	US-09-968-362-20	Seguence 20,	ADI
m	566.5	97.2	472	14	US-10-006-593-67	Seguence 67,	Apr
4	566.5	97.2	472	15	US-10-307-724-67		Apr
ഹ	565	96.9	218	12	US-09-813-341-5	2	Appl
9	565	6.96	218	14	US-10-277-307-5	'n	Appl
7	565	96.9	218	14	US-10-277-370-5	Sequence 5, 7	Appl
æ	565	96.9	218	14	US-10-196-394-76	Sequence 76,	Apr
ďη	565	6.96	218	15	US-10-370-749-18	Sequence 18,	Apr
10	565	6.96	284	12	US-10-433-108-24	Sequence 24,	Apr
11	565	96.9	327		US-09-925-664-47	Sequence 47,	Appl
12	565	96.9	327		US-10-047-542-26	Sequence 26,	Apr
13	565	6.96	327		US-10-310-719-7	Sequence 7, 1	Appl
14	565	96.9	327		US-10-112-582-4	Sequence 4, 7	Appl
15	565	6,96	329	σ	US-09-935-868-12		Appl

Sequence 100, App Sequence 12, Appl Sequence 12, Appl Sequence 169, App	L- 1-1 CA	4 28	4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	Sequence 60, Appl Sequence 52, Appl Sequence 52, Appl Sequence 54, Appl Sequence 52, Appl Sequence 54, Appl Sequence 54, Appl
10 US-09-990-586-100 14 US-10-287-035-12 14 US-10-287-162-12 14 US-10-310-113-169 14 US-10-230-880-100	US-10-050-227-7 US-10-050-227-1 US-09-859-361-2 US-09-859-361-5 US-10-005-438-2	- S - S - S - S - S - S - S - S - S - S	14 US-10-211-357-12 15 US-10-428-408A-30 9 US-09-935-868-46 19 US-09-935-868-50 14 US-10-287-035-46 14 US-10-287-035-50 14 US-10-287-035-56	
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	4 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	467 778 778 778 778	778 782 782 782 782
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ALIGNMENTS

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DEPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Bill N
APPLICANT: Sun, Bill N
APPLICANT: Sun, Ceily R
TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biolog FILE REFERENCE: 025UNZ001
CURRENT APPLICATION NUMBER: US/09/932,812
CURRENT FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: HuBPO-L-vPc gamma4 with a 27-amino acid leader peptide (Figure 2 US-09-932-812-20
                      ; Sequence 20, Application US/09932812; Publication No. US20030082749A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
US-09-932-812-20
```

ö 1 APPVAGGESVFLFPPKPKDTLMISRIPEVICVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60 0; Gaps 97.8%; Score 570; DB 10; Length 437; 98.2%; Pred. No. 4.8e-50; tive 0; Mismatches 2; Indels (Query Match
Best Local Similarity 98.2 Matches 108; Conservative В

61 PREEQPNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIBKTISKAK 110 281 PRESQENSTYRVVSVLTVLHQDMLNGKEYKCKVSNKGLPSSIEKTISKAK 330 ò 용

RESULT 2 US-09-968-362-20

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257 APPVA-GPSVPLFPPKPKDTLMISRTPEVTCVVVDVSQEDPSVQENWYVDGVEVHNAKTK 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-09-813-31-5
Squence 5, Application US/09813341
Squence 5, Application US/09813341
Squence 5, Application Wo. US20020004587A1
GENERAL INPORMATION:
THE GENERAL INPORMATION:
TITLE OF INVENTION: WULTIVALENT ANTIBODIES AND USES THEREFOR TITLE EPERRANCE: P1780R1
CURRENT FILING DATE: 2001-03-20
PRIOR PAPLICATION NUMBER: US 60/195,819
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 11
SSEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 15; Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 218;
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                                                                                                                                                                       PUDLICATION NO. US200302329/7241

GENERAL INFORMATION:
APPLICANT: Brade:icksor, Shana
APPLICANT: Erede:icksor, Shana
APPLICANT: Rendericksor, Shana
APPLICANTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2619
CURRENT APPLICATION NUMBER: US 60/291,448
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2000-12-05
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-05
PRIOR APPLICATION NUMBER: US 10/006,593
PRIOR FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 134
SOFTWARE: PATENTIN UNIVERER: US 10/006,593
FRIOR FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 134
SEG ID NO S: 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query March 97.2%; Score 566.5; DB 15;
Best Local Similarity 99.1%; Pred. No. 1.2e-49;
Matches 109; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 96.9%; Score 565; DB 12; Best Local Similarity 97.3%; Pred. No. 6.8e-50; Matches 107; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) OTHER INFORMATION: Humanized antibody heavy chain US-10-307-724-67
                                                                                  RESULT 4
US-10-307-724-67
Sequence 67, Application US/10307724
; Publication No. US20030232972A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CRCANISM: Homo sapiens
US-09-813-341-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ਨੇ
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Sequence 20, Application US/09968362
Publication No. US20030082679A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sun, Bill
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulaing factor
TITLE OF INVENTION: biological activities
FILE REFERENCE: 035U02001
FILE REFERENCE: 035U02001
CURRENT APPLICANT: 2001-10-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: hG-CSF-L-vFc gamma4 with a 30-amino acid leader peptide (Figure CTHER INFORMATION: B) US-09-968-362-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257 APPVA-GPSVFLFPPKFKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVNAKTK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 APEFAGGESVFLFPPFKEKDTLMISRIPEVTCVVVDVSQEDPEVQENWYDGVEVNRAKTK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 APPVAGGPSVFLFPPKPKDTLMISRTPEVICVVVDVSQBDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PREEGENSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 570; DB 10; Length 4
Pred. No. 4.9e-50;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 67, Application US/10006593

Sequence 67, Application US/10006593

Publication No. US20030049663A1

GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Renshaw, Mark
TITLE OF INVAITION: RATIONALLY DESIGNED ANTIBODIES
FILE REPRENCE: 1087-2
CURRENT APPLICATION NUMBER: US/10/006,593
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2010-05-04
PRIOR FILING DATE: 2010-05-04
PRIOR FILING DATE: 2010-05-04
SPRIOR FILING DATE: 2010-05-05
SOFTWARE: PALENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Humanized antibody heavy chain US-10-006-593-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 97.8%;
Best Local Similarity 98.2%;
Matches 108; Conservative
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US-10-006-593-67
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1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60 2 APEFLGGPSVFLFPPKPKDTLMISRIPEVICVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 61 1 APPVAGGPSVPLFPPKPFLMISRTPEVTCVVVDVSQEDFEVQFNWYVDGVEVHNAKTK 60 2 APEFLGGPSVFLFPPKDTLMISRTPEVTCVVVDVSQEDPEVQFVWYVDGVEVHNAKTK 61 O, Gaps 0; Gaps 61 PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110 62 PREEQENSTYRVVSVLTVIHQDWINGKEYKCKVSNKGLPSSIEKTISKAK 111 61 PREBOFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAR 110 62 PREBQFNSTYRVVSVITVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 111 Query March 96.9%; Score 565; DB 14; Length 218; Best Local Similarity 97.3%; Pred. No. 6.88-59; Marches 107; Conservative 0; Mismarches 3; Indels 6 Query Match

96.9%; Score 565; DB 14; Length 218;

Best Local Similarity 97.3%; Pred. No. 6.8e-50;

Matches 107; Conservative 0; Mismatches 3; Indels (APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Glycoprotein Compositions
FILE REFERENCE: 118771
CURENT APPLICATION NUMBER: US/10/277,307
CURENT FILING DATE: 2002-10-22
PRIOR FILING DATE: 2001-10-25
PRIOR FILING DATE: 2001-10-25
PRIOR FILING DATE: 2001-10-25
NUMBER OF SEQ ID NOS: 9
SEQ ID NO S. APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Glycoprotein Compositions
FILE REFERENCE: 1913771
CURRANT APPLICATION NUMBER: US/10/277,370
CURRANT FILING DATE: 2003-02-10
FRIOR APPLICATION NUMBER: US 60/337,642
PRIOR APPLICATION NUMBER: US 60/347,694
FRIOR APPLICATION NUMBER: US 60/347,694
FRIOR APPLICATION NUMBER: US 60/347,694
FRIOR PILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 5 US-10-277-307-5 ; Sequence 5. Application US/10277307 ; Publication No. US20030139908A1 ; GENERAL INFORMATION: ; Sequence 5, Application US/10277370 ; Publication No. US20030157108A1 ; GENERAL INFORMATION: TYPE; PRT ORGANISM: homo sapiens TYPE: PRT ORGANISM: homo sapiens LENGTH: 218 US-10-277-307-5 US-10-277-370-5 LENGIH: 218 ; UKS-10-277-370-5 8 셤 ð g ઠે

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Gaps

o O

Query Match 96.9%; Score 565; DB 14; Length 218; Best Local Similarity 97.3%; Pred. No. 6.8e-50; Matches 107; Conservative 0; Mismatches 3; Indels (

TYPE: PRT ORGANISM: Homo sapiens

US-10-196-394-76

US-10-196-394-76
Sequence 76, Application US/10196394
Publication No. US20030171278A1
GENERAL INFORMATION:
APPLICANT: MAT'K S. Dennis
TITLE OF INVENTION: Compounds that Bind HBR2
FILE REFERENCE: P1713R1
CURRENT APPLICATION NUMBER: US/10/196,394
CURRENT FILING DATE: 2002-07-15
PRIOR PLILING DATE: 2000-06-30
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 76
LENGTH: 218

RESULT 8

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1 APPVAGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 APEFLGGPSVFLFPPKPKDTLÆISRTPEVTCVVVDVSQBDPEVQFNWYVDGVEVHNAKTK 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 96.9%; Score 565; DB 15; Length 218; Best Local Similarity 97.3%; Pred. No. 6.8e-50; Matches 107; Conservative 0; Mismatches 3; Indels 0
                                                                                                                                  APPLICANT: Watkins, Jeffry D.
APPLICANT: Watkins, Jeffry D.
APPLICANT: Allan, Barrett
TITLE OF INVENTION: FC Region Variants
FILE REFERENCE: AME-078.2
CURRENT APPLICATION NUMBER: US/10/370,749
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/358,161
PRIOR FILLING DATE: 2002-02-20
NUMBER OF SEQ ID NOS: 54
                                                   Sequence 18, Application US/10370749; Publication No. US20040002587A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin version 3.2
SEQ ID NO 18
LENGTH: 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
RESULT 9
US-10-370-749-18
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Sequence 24, Application US/10433108; Publication No. US20040053370A1

RESULT 10 US-10-433-108-24

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68 APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDFBVQFNWYVDGVEVHNAKTK 127
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| Sequence 47, Application US/09925664
| Patent No. US20020160006A1
| GENERAL INFORMATION:
| APPLICANT: Denney, Ur., Dan W. APPLICANT: Denney, Ur., Dan W. TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia TITLE OF INVENTION: WHENCE O6499
| TITLE OF INVENTION: WHENCE US/09/925,664
| CURRENT APPLICATION NUMBER: US/09/925,664
| PRIOR PILING DATE: 1999-08-09
| PRIOR APPLICATION NUMBER: 08/644,664
| PRIOR PILING DATE: 1996-05-01
| PRIOR FILING DATE: 1996-05-101
| PRIOR FILING DATE: 1996-05-10-106
| NUMBER OF SEQ ID NOS: 80
| SOFTWARE: PatentIn Version 3.1
| LENGTH: DATE OF THE OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

96.9%; Score 565; DB 12; Length 284;
Best Local Similarity 97.3%; Pred. No. 9.3e-50;
Matches 107; Conservative 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 327
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96.9%; Score 565; DB 9;
Best Local Similarity 97.3%; Pred. No. 1.1e-49;
Matches 107; Conservative 0; Mismatches 3.
APPLICANT: B11 Lilly and Company
TITLE OF INVENTION: GLP-1 FUSION PROTEINS
FILE REPERENCE: X-13991
CURRENT APPLICATION NUMBER: US/10/433,108
CURRENT FILING DATE: 2003-05-29
PRIOR PILING DATE: 2003-05-10
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Petentin version 3:1
SOFTWARE: Petentin version 3:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: synthetic construct US-10-433-108-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CRGANISM: Homo sapiens
US-09-925-664-47
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US-09-925-664-47
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1 APPVAGGPSVFLFPPKPKDTLMISRIPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK

Query Match 96.9%; Score 565; DB 13; Length 327; Best Local Similarity 97.3%; Pred. No. 1.1e-49; Matches 107; Conservative 0; Mismatches 3; Indels (

ORGANISM: Homo sapiens US-10-047-542-26

TYPE: PRT

0; Gaps

APPLICANT: LARRICK, JAMES W.
APPLICANT: WYCOFF, KBITH L.
TITLE OF INVENTION: NOVEL BATTHLALD ISBASES
TITLE OF INVENTION: NOVEL BATTHLALD ISBASES
FILE REFERENCE: 030905.0004.CTP1
CURRENT PELLING NUMBER: US/A/O/47,542
CURRENT FILING DATE: 2001-10.26
PRIOR PILING DATE: 2001-10.28
PRIOR PELICATION NUMBER: 60/200,298
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
SEQ ID NOS: 101
SOFTWARE DATE: 2000-04-28
SEQ ID NOS: 101
SSEQ ID NOS: 201
LENGTH: 327

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1 APPVAGGPSVFLFPPKKPKDTLMISRIPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
US-10-310-719-7

Sequence 7, Application US/10310719

Sequence 7, Application US/10310719

Publication No. US20030166163A1

GENERAL INFORMATION:
TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
TITLE REPERENCE: LEX-020

CURRENT APPLICATION NUMBER: US/10/310,719

CURRENT FILING DATE: 2002-12-04

PRIOR APPLICATION NUMBER: 60/337,113

PRIOR PILING DATE: 2002-04-12

PRIOR PILING DATE: 2002-04-12

NUMBER OF SEQ ID NOS: 37

SEQ ID NO 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PREEQENSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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97.3%; Pred. No. 1.1e-49;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KBY: misc
i_LOCATION: (1)...(327)
CTHER INFORMATION: Human gamma 4 constant region
US-10-310-719-7
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Best Local Similarity 97.33
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                          LENGTH: 327
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RESULT 14 US-10-112-582-4

; Sequence 26, Application US/10047542; Publication No. US20020168367A1; GENERAL INFORMATION:

RESULT 12 US-10-047-542-26

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RESULT 15
US-09-35-568-12
Sequence 12, Application US/09935868
Sequence 12, Application US/09935868
Sequence 12, Application US/09935868
Sequence 12, Application US/09935868
Fatent No. US20020164690A1
FIRENERAL ENGRAPHICANT: Regeneron Pharmaceuticals, Inc
TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
FILE REPERRINCE: REG 2019
CURRENT APPLICATION WUMBER: US/09/935,868
CURRENT FILING DATE: 1099-09-11
FRIOR PILING DATE: 1099-09-22
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
LENGTH: 329
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; Sequence 4, Application US/10112582; Publication No. US20030166877A1; GENERAL INFORMATION: GENERAL INFORMATION: Stephen; TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins; TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins; FILE REPERENCE: LEX-017 CURRENT APPLICATION NUMBER: US/10/112,582; CURRENT FILING DATE: 2002-03-29; PRIOR PILING DATE: 2001-03-30; NUMBER: OF SEQ ID NOS: 59; SOFTWARE: Patentin version 3.0; SEQ ID NO 4; SEQ ID NO 4
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96.9%; Score 565; DB 9; Length 329;
Best Local Similarity 97.3%; Pred. No. 1.1e-49;
Matches 107; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
OTHER INFORMATION: Ig gamma-4 chain C region
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US-09-935-868-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM:
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Search completed: April 29, 2004, 08:55:55 Job time : 39.5 sec8

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Thu Apr 29 09:15:44 2004
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TB-03-6/4-60/E-80

542 542 542.	33 542.5 34 542.5 35 542.5 36 542.5 36 542.5 36 542.5 37 542.5	542.	542.	1		RESULT 1 IIS-08-444-644-44	Sequence 44, A. Patent No. 601, GENERAL INFOR.	TITLE OF IN TOTAL OF IN TOTAL OF IN TOTAL OF IN TITLE OF IN	STATE: STATE: COUNTRY: 1 21P: 021	COMPUTER:	SOPTWARE:	APPLICATI	CLASSIFIC	APPLICATI	FILING DA	APPLICATE	FILING DA	, APPLICATI	; FILLING DA ; PRIOR APPLI	, APPLICATI	: ATTORNEY/AG	REGISTRAT	TELECOMMUNI	TELEFACE: TELEFAX: TNEODMATTON B	SEQUENCE CH.	; LENGIH: ; TYPE: am	10101011
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	OM protein - protein search, using sw model Run on: April 29, 2004, 08:42:33 ; Search time 16.5 Seconds (without alignments) 344.173 Million cell updates/sec	Title: US-09-674-857-12 Perfect score: 583 Sequence: 1 APPVAGGPSVFLFPFKDTCKVSNKGLPSSIEKTISKAK 110	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 389414 segs, 51625971 residues	Total number of hits satisfying chosen parameters: 389414	Minimum DB seq length: 0 Maximum DB seq length: 20000000000	Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries	Database: Issued_Patents_AA:* 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:* 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:* 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:* 4: /cgn2_6/ptodata/2/iaa/B_COMB.pep:* 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:* 6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		Result No. Score Match Length DB ID	96.9 110 3 US-08-444-644-44 Sequence 44	96.9 327 2 US-08-761-277A-47 Sequence 47	565 96.9 329 4 US-09-313-942-12 Sequence 12	96.9 382 1 US-08-470-299-10 Sequence 10	565 96.9 443 5 PCT-US96-13152-4 Sequence 4,	565 96.9 467 2 US-07-916-098A-45 Sequence 45	565 96,9 467 3 US-08-523-894-8 Sequence B, 565 96.9 467 3 US-08-523-894-10 Sequence 10	565 96.9 467 3 US-08-523-894-12 Sequence 12	561 96.2 109 4 US-08-557-050-4 Sequence 4,	559 95.9 328 3 US-08-808-720-1 Sequence 5.	559 95.9 331 3 US-08-808-720-7 Sequence 7.	559 95.9 374 4 US-09-227-595-28 Sequence 28	546 93.7 468 4 US-09-495-7378-67 Sequence 6 546 93.7 488 4 US-09-499-861.12 Sequence 1	93.7 497 4 US-09-499-846-10 Sequence 10	546 93.7 711 4 US-09-485-7378-90 Sequence 90 542.5 93.1 109 3 US-08-444-644-30 Sequence 30 542.5 93.1 93.1 93.1 93.1 93.1 93.1 93.1 93.1	542.5 93.1 109 4 US-08-232-246A-30 Sequence 30,

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44-44
44, Application US/08444644
16. Application US/08444644
1. 6015555
1. 1020AMATION:
ANT: Friden, Phillip M.
ANT: Friden, Phillip M.
OF INVENTION: TRANSFERIN RECEPTOR SPECIFIC
OF INVENTION: CONJUGATES
OF SOURNCES: 46
PONDENCE ADDRESS:
ESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
EST: Two Militia Drive
1: Lexington
1: Lexington
1: Lexington
1: USA
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RESULT 4
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                                                                                                                                                                                                         1 APEFLGGESVFLFFPKENDTLMISTTPEVTCVVVDVSQEDBEVQFNWYVDGVEVHNAKTK 60
                                                                                                                                                                                 1 APPVAGGESVFLFPPKEKDTLMISKTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: COMJUGATES
NUMBER OF SEQUENCES: 46
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                      61 PREEQPINSTYRVUSVLTVIHOUMINGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                           PREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                     Query Match 96.9%; Score 565; DB 3; Length 110; Best Local Similarity 97.3%; Pred. No. 9.6e-61; Matches 107; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATION SYSTEM:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/23,246A
FILING DATE: 0-04-MAY-1994
CLASSIFICATION NUMBER: US/08/23,246A
FILING DATE: 0-04-MAY-1994
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US/7/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1999
ATPONEY/AGENT INPORMATION:
NAME: WAGJUET, RICHARD W.
REGISTRATION NUMBER: 34,480
REGISTRATION NUMBER: 34,480
REGISTRATION NUMBER: ALK88-15AAA
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 44, Application US/08232246A
Patent No. 6329508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 110 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 97.3
Matches 107; Conservative
    protein
internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lexington
MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-232-246A-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-232-246A-44
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                                              US-08-444-644-44
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1 APPVAGGPSVFLPPPKPKDYLMISRTPEVTCVVVDYSQEDPEVQFNWYVDGVEVHNAKTK 60

0; Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-313-942-12
Sequence 12, Application US/09313942
Fatent No. 6472179
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: ARCEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
TITLE OF INVENTION: AND USING
FILE REPERENCE: REG 203-A
                                                                                                                                                                                                             61 PREEQFNSTYRVVSVLTVLHQDWINGKEYKCKVSNKGLPSSIBKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PREEDENSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.9%; Score 565; DB 2; Length 327; 97.3%; Pred. No. 4.2e-60; Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentla Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,277A
FILING DATE: 06-DEC-1996
CLASSIFICATION: A24
PRIOR APPLICATION: DATA:
APPLICATION NUMBER: US/08/644,664
FILING DATE: 01-0AR-1996
ATTORNEY/AGRNT INFORMATION:
NAME: MacKnight, Ramin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: GENITOPE-02406
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
THERPHOME: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 97.3
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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Thu Apr 29 09:15:44 2004

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113 APEFLGGPSVFLPPPRENDILMISRIPBVTCVVVDVSQEDPEVQFNWYVDGVEVENAKIK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PREBQFNSTYRVVSVLTVLHQDWLWGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                     Query Match 96.9%; Score 565; DB 4; Length 329; Best Local Similarity 97.3%; Pred. No. 4.3e-60; Matches 107; Conservative 0; Mismatches 3; Indels
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Pred. No. 5.2e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patencin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,299
FILING DATE: 06-JUN-1995
CLASSIPICATION: 435
ATTORNEY/AGENT INPORMATION:
NUMBE: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REPERENCE/DOCKET NUMBER: P31005C3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 5090
INPORMATION FOR SEQ ID NO: 7:
SEQUENCE CRARACTERISTICS:
LENGTH: 382 amino acids
TUDENGTH: 382 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08470299
Facence 7, Application US/08470299
Facence 7, Application US/08470299
Facence 7, Application
GENERAL INFORMATION:
APPLICANT: Browne, Michael J.
APPLICANT: Chapman, Conrad G.
APPLICANT: Clinkenbeard, Helen E.
APPLICANT: Young, Peter R.
APPLICANT: Young, Peter R.
APPLICANT: Shatzman, Allan R.
TITLE OF INVENTION: No. 5783181el Compounds
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 709 Swedeland Road, P.O. Box 1539 CITY: King of Prussia STATE: Pennsylvania COUNTRY: USA
CURRENT APPLICATION NUMBER: US/09/313,942
CURRENT FILING DATE: 1999-05-19
FRIOR APPLICATION NUMBER: 09/313,942
FRIOR PILING DATE: 1999-05-19
FRIOR PELING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 329
TYPE: RRT
TYPE: RRT
USGANISM: Homo sapiens
US-09-313-942-12
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Best Local Similarity
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US-08-470-299-7
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1 APPVAGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60
Gaps
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                                                                                                                                                                                                                                                                                          226 PREEGENSTYRVVSVLTVLHODWLNGKEYKCKVSNKGLESSIEKTISKAK 275
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96.9%; Score 565; DB 1; Length 38

Best Local Similarity 97.3%; Pred. No. 5.2e-60;

Matches 107; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER FEADMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,299
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATCARSIFICATION NUMBER: 34,028
RECENTATION NUMBER: 34,028
REGRENCE/DOCKET NUMBER: 921005C3
FILEDFACTION NUMBER: 191005C3
FILEDFACTION NUMBER: 1910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/08470299
Sequence 10, Application US/08470299
Patent No. 5783181
GENERAL INFORMATION:
APPLICANT: Murphy, Kay E.
APPLICANT: Clinkenbeard, Helen E.
APPLICANT: Clinkenbeard, Helen E.
APPLICANT: Shatzman, Allan R.
TITLE OF INVENTION: No. 5783181e1 Compounds
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: SmithKilne Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
STATE: Pennsylvania
    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
PCT-US96-13152-4
; Sequence 4, Application PC/TUS9613152
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich, et al.
        107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
US-08-470-299-10
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US-08-470-299-10
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        Matches
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WESULY 9

WESULY 19

WESULY 10

WESUL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 APPVAGGPSVFLEPPKEDTLMISRIPEVICVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PREBQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

96.9%; Score 565; DB 1; Length 467;
Best Local Similarity 97.3%; Pred. No. 6.9e-60;
Matches 107; Conservative 0; Mismatches 3; Indels
COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Macintosh
SOSTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,744
FILING DATE: 06-SEPT-1996
CLASSIPICATION NUMBER: US 08/20886
FILING DATE: 10-MAR-1994
APPLICATION NUMBER: PCT/US/95/02400
FILING DATE: 10-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: FOULKe, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: JB0429K
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELESPAX: (908) 298-2987
TELERAX: 1008 298-5388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
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CORRESPONDENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Felfe & Lynch
ADDRESSER: Attn: Norman D. Hanson
STREET: 805 Third Avenue
CITY: New York
CUNTX: U.S.A.
COUNTX: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: NOSYMS-DOS
COMPUTER: NOSYMS-DOS
COMPUTER: NOSYMS-DOS
COMPUTER: NOSYMS-DOS
COMPUTER: NOSYMS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287 PREEGPNSTYRVVSVLTVLAQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

96.9%; Score 565; DB 5; Length 443;
Best Local Similarity 97.3%; Pred. No. 6.4e-60;
Matches 107; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

CURRENT APPLICATION NUMBER: PCT/US96/13152
FILING DATE:

PRIOR APPLICATION NUMBER: PCT/US96/13152
FILING DATE: 27-Dec-95
APPLICATION NUMBER: BP 95 112 895.8
FILING DATE: 17-Aug-95
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
ATTORNEY/AGENT INFORMATION:

NAME: WORMAN DECENT NUMBER: BORE 1059-PCT-PFF/NDH
TELECOMMUNICATION NUMBER: BORE 1059-PCT-PFF/NDH
TELECOMMUNICATION INFORMATION:
TELEPRAX: (212) 688-9200
TELEPRAX: (212) 838-3884
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDENNESS: double
TOPOLOGY: linear
MOLECTLE TYPE: protein
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 APPVAGGPSVFLFPPKPKDTLMISRTPBVTCVVVDVSQEDPBVQFNWYVDGVBVHNAKTK 60
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US-08-53-894-8

| Sequence 8, Application US/08523894
| Patent No. 6136310
| GTRERAL INFORMATION:
| APPLICANT: Hearina, Nabil APPLICANT: Newman, Roland A. APPLICANT: Reff. Mitchell E. TITLE OF INVENTION: Therapy Recombinant Anti-CD4 Antibodies for Human TITLE OF INVENTION: Therapy NUMBER OF SEQUENCES: 59
| CORRESPONDENCE ADDRESS: ADDRESSER: 699 Prince Street CITY: Alexandria STREET: 699 Prince Street CITY: Alexandria STATE: WA COUNTY: USA
| COMPUTER READABLE FORM: MEDIA STATE: WA CONFUTER READABLE FORM: MEDIA STATE: US OF WARAE: PREPRICATION NUMBER: US/08/523,894
| COMPUTER READABLE FORM: MEDIA STATE: US/08/523,894
| CURRENT APPLICATION NUMBER: US/08/523,894
| PILMO DATE: O6-SEP-1995 | CLASSIFICATION NUMBER: 35,030 | REFERENCE/DOCKET NUMBER: 35,030 | REFERENCE/DOCKET NUMBER: 35,030 | REFERENCE/DOCKET NUMBER: 35,030 | REFERENCE/DOCKET NUMBER: 35,030 | TELECOMMUTCATION: NOT OF 18 NOT O
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APPLICATION NUMBER: PCT/US91/08843
FILING DATE: No. 5871732ember 27, 1991
CLASSIFICATION: 424
APPLICATION: 424
APPLICATION: WHERE: 07/618,542
FILING DATE: No. 5871732ember 27, 1990
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: JOHN J. MC DONNELL
REGISTRATION NUMBER: 92,310-G
TELECOMNUNICATION INFORMATION:
TELECOMNUNICATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFOR
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INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein US-07-916-098A-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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251 APEFEGGESVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHAKTK 310
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                                                                                                                                                                                                                                                                                                                              1 APPVAGGPSVFLFPPKPTTMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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Sequence 10, Application US/08523894

Patent No. 6136110

GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Newman, Roland A.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
TITLE OF INVENTION: Therapy
TOCRESPONDENCE ADDRESS:
ADDRESSEE: UNROWNION: SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STRIES 'VA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PREEQFNSTYRVVSVLTTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAK 110
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                                                                                                                                                             Ouery Match
Best Local Similarity 97.3%; Pred. No. 6.9e-60;
Matches 107; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRL.
STATE: VA
STATE: VA
STATE: VA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: EACH STATE: CONTROLL
CONFUTER: ENDOY disk
COMPUTER: ENDOY disk
COMPUTER: ENDOY WISK
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRATING SYSTEM: PC-DOS/MS-DOS
CURRATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995
CLASSIFICATION NUMBER: US/08/523,894
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHOME: 703-836-2021
TELECHOME: 703-836-2021
TELEPAX: NOB-886-2021
TELEPAX: ACIGS
COUNTRY AGENT INFORMATION:
TELEPAX: ACIGS
TELEPAX: ACIGS
COUNTRY AGENT INFORMATION:
TOWN SEQ ID NO: 10:
TELEPAX: ACIGS
COUNTRY AGENT INFORMATION:
ACIGS
COUNTRY AGENT INFORMATION:
TOWN AGENT INFORMATION:
ACIGS
COUNTRY AGEN
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-523-894-8
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US-08-523-894-10
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Sequence 12.2.934-12
Sequence 12.3 Application US/08523894
Sequence 12.3 Application US/08523894
Settle No. 6136310
GENERAL INFORMATION:
APPLICANT: Heama, Nabil
APPLICANT: Newman, Roland A.
SAPLICANT: Newman, Roland A.
TITLE OF INVENTION: Therapy
INTERE OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
COUNTRY: USA
STATE: PRACHE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIOS STREE: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
STREET: READENT: OG-SEP-1995
SOFTWARE: PATENT NOBER: 10508523,894
FILING DATE: OG-SEP-1995
STRING DATE: TOJ-836-620
STRIERAX: 703-836-620
STRIERAX: 703-836-6301
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APPLICANT: Zivin, Robert A.
APPLICANT: Zivin, Robert A.
APPLICANT: Zivin, Robert A.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Bluestone, Jeffrey A.
TITLE OF INVENTION: Methods and Materials For Modulation
TITLE OF INVENTION: Of the Immuno-suppressive Activity and
TITLE OF INVENTION: Toxicity of Monoclonal Antibodies
NUMBER OF SEQUENCES: 18
CORRESPENDINGER ADDRESS:
ADDRESSES: Arnold, White & Durkee
STREET: P.O. 30x 4433
CITY: Houston
STREET: P.O. 30x 4433
CITY: Houston
STREET: Texas
COUNTRY: United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 96.9%; Score 565; DB 3; Length 467; Best Local Similarity 97.3%; Pred. No. 6.9e-60; Matches 107; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
US-08-070-116A-4
; Sequence 4, Application US/08070116A
; Parent No. 5885573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-523-894-12
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RESULT 14

US-08-557-050-4

US-08-557-050-4

US-08-557-050-6

Sequence 4, Application US/08557050

Patent No. 6451916

CENERAL INFORMATION:
APPLICANT: Elucation Jeffrey A. APPLICANT: APPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 PEFLGGESVFLFPPRENDTLMISKTPEVTCVVVDVSQEDFBVQFNWYVDGVEVHNAKTKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 PPVACGPSVFLPPPKPKDTLMISRTPBVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

96.2%; Score 561; DB 2;
Best Local Similarity 97.2%; Pred. No. 2.9e-60;
Matches 106; Conservative 0; Mismatches 3.
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/070,116A
PILING DATE: 01-JUN-1993
CLASSIFICATION NUMBER: 37,259
REPERENCY INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REPERENCY DOCKET NUMBER: 37,259
REPERENCY FOR THE B.
REGISTRATION NUMBER: 37,259
REPERENCY FOR THE B.
REGISTRATION NUMBER: 37,259
REPERENCY FOR THE B.
REGISTRATION OF SEQ 10 NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
```

61 1 PEFLGGPSVFLPPPKDKDTLMISRIPEVTCVVVDVSQEDPEVQFNWYDGVBVBVAKTKP 60 2 PPVAGGESVFLFPPKFKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 0; Gaps 62 REBOPNSTYRVVSVLTVLHODWLNGKEYKCKVSNKGLPSSIEKTISKAK 110 Query March 96.2%; Score 561; DB 4; Length 109; Best Local Similarity 97.2%; Pred. No. 2.9e-60; Matches 106; Conservative 0; Mismatches 3; Indels

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61 REEQFNSTYRVVSVLTVLHQDWLNGKEYXCKVSNKGLPSSIEKTISKAK 109 원

RESULT 15
US-08-808-720-3
is Sequence 3, Application US/08808720
; Sequence 3, Application US/08808720
; RETENT No. 6100347;
; GENERAL INFORMATION:
APPLICANT: Hermann, Steve
ITILE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING
ITILE OF INVENTION: CHEMORIC POLYPEPTIDES CONTAINING
ITILE OF INVENTION: CHEMORIC DOMAINS
CORRESPONDENCES: 10
CORRESPONDENCES: 10
STREET: 87 CambridgePark
CITY: Cambridge
CITY: MA CITY: Cambridge
STATE: MA
ZIP: Cambridge
STATE: MA
ZIP: 0240
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,720
FILING DATE:
CLASSITCATION NUMBER: D-41,323
REGISTRATION NUMBER: P-41,323
REFERENCE/DOCKET NUMBER: P-41,323
REGISTRATION INFORMATION:
TELECOMMUNICATION OF 3:
SEQUENCE CHARACTERISTICS:
LEMOTH: 236 mmino acids
LEMOTH: 236 mmino acids

Query Match 95.9%; Score 559; DB 3; Length 326; Best Local Similarity 96.4%; Pred. No. 2.3e-59; Matches 106; Conservative 0; Mismatches 4; Indels i: 326 amino acids amino acid , TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-808-720-3 STRANDEDNESS:

1 APPVAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTK 60

Search completed: April 29, 2004, 08:47:44 Job time : 17.5 secs